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(71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).

(72) Inventors; and
(75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).

(74) Agents: GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).

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(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele–specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

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BIALLELIC MARKERS

RELATED APPLICATIONS
    This application claims priority to U.S. provisional
application Serial No. 60/030,455, filed November 6, 1996,
5 the entire teachings of which are incorporated herein by
reference.

BACKGROUND OF THE INVENTION
    The genomes of all organisms undergo spontaneous
mutation in the course of their continuing evolution,
10 generating variant forms of progenitor sequences (Gusella,
Ann. Rev. Biochem. 55, 831-854 (1986)). The variant form
may confer an evolutionary advantage or disadvantage
relative to a progenitor form or may be neutral. In some
instances, a variant form confers a lethal disadvantage and
15 is not transmitted to subsequent generations of the
organism. In other instances, a variant form confers an
evolutionary advantage to the species and is eventually
incorporated into the DNA of many or most members of the
species and effectively becomes the progenitor form. In
20 many instances, both progenitor and variant form(s) survive
and co-exist in a species population. The coexistence of
multiple forms of a sequence gives rise to polymorphisms.
    Several different types of polymorphism have been
reported. A restriction fragment length polymorphism
25 (RFLP) Is a variation in DNA sequence that alters the
length of a restriction fragment (Botstein *et al.*, *Am. J.
Hum. Genet.* 32, 314-331 (1980)). The restriction fragment
length polymorphism may create or delete a restriction
site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic
analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell*
51, 319-337 (1987); Lander *et al.*, *Genetics* 121, 85-99
(1989)). When a heritable trait can be linked to a
5   particular RFLP, the presence of the RFLP in an individual
can be used to predict the likelihood that the animal will
also exhibit the trait.

Other polymorphisms take the form of short tandem
repeats (STRs) that include tandem di-, tri- and tetra-
10 nucleotide repeated motifs. These tandem repeats are also
referred to as variable number tandem repeat (VNTR)
polymorphisms. VNTRs have been used in identity and
paternity analysis (US 5,075,217; Armour *et al.*, *FEBS Lett.*
307, 113-115 (1992); Horn *et al.*, WO 91/14003; Jeffreys, EP
15 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide
variations between individuals of the same species. Such
polymorphisms are far more frequent than RFLPs, STRs and
VNTRs. Some single nucleotide polymorphisms occur in
20 protein-coding sequences, in which case, one of the
polymorphic forms may give rise to the expression of a
defective or other variant protein and, potentially, a
genetic disease. Examples of genes, in which polymorphisms
within coding sequences give rise to genetic disease
25 include β-globin (sickle cell anemia) and CFTR (cystic
fibrosis). Other single nucleotide polymorphisms occur in
noncoding regions. Some of these polymorphisms may also
result in defective protein expression (e.g., as a result
of defective splicing). Other single nucleotide
30 polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same
manner as RFLPs and VNTRs, but offer several advantages.
Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the
genome than other forms of polymorphism.   The greater
frequency and uniformity of single nucleotide polymorphisms
means that there is a greater probability that such a
5 polymorphism will be found in close proximity to a genetic
locus of interest than would be the case for other
polymorphisms.   The different forms of characterized single
nucleotide polymorphisms are often easier to distinguish
than other types of polymorphism (e.g., by use of assays
10 employing allele-specific hybridization probes or primers).
       Only a small percentage of the total repository of
polymorphisms in humans and other organisms has been
identified.   The limited number of polymorphisms identified
to date is due to the large amount of work required for
15 their detection by conventional methods.   For example, a
conventional approach to identifying polymorphisms might be
to sequence the same stretch of DNA in a population of
individuals by dideoxy sequencing.   In this type of
approach, the amount of work increases in proportion to
20 both the length of sequence and the number of individuals
in a population and becomes impractical for large stretches
of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a
5   polymorphic site. Complements of these segments are also included.   The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying
10   the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base .(Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These
15   oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table,
20   column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a
25   set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases
30   present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or
double-stranded. Oligonucleotides can be naturally
5   occurring or synthetic, but are typically prepared by
synthetic means. The oligonucleotides of the present
invention can comprise all of an oligonucleotide sequence
presented in column 7 of the Table or a segment of such an
oligonucleotide which includes a polymorphic site.
10   Oligonucleotides can be all of a nucleic acid segment as
represented in column 7 of the Table; a nucleic acid
sequence which comprises a nucleic acid segment represented
in column 7 of the Table and additional nucleic acids
(present at either or both ends of a nucleic acid segment
15   of column 7); or a portion (fragment) of a nucleic acid
segment represented in column 7 of the Table which includes
a polymorphic site. Preferred oligonucleotides of the
invention include segments of DNA, or their complements,
which include any one of the polymorphic sites shown in the
20   Table. The segments can be between 5 and 250 bases, and,
in specific embodiments, are between 5-10, 5-20, 10-20, 10-
50, 20-50 or 10-100 bases. The polymorphic site can occur
within any position of the segment. The segments can be
from any of the allelic forms of DNA shown in the Table.
25   Hybridization probes are oligonucleotides which bind in
a base-specific manner to a complementary strand of nucleic
acid. Such probes include peptide nucleic acids, as
described in Nielsen et al., Science 254, 1497-1500 (1991).
As used herein, the term primer refers to a single-
30   stranded oligonucleotide which acts as a point of
initiation of template-directed DNA synthesis under
appropriate conditions (e.g., in the presence of four
different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from

5   15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

    As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

    As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site

25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified
allelic form is arbitrarily designated as the reference
form and other allelic forms are designated as alternative
or variant alleles. The allelic form occurring most
5   frequently in a selected population is sometimes referred
to as the wildtype form. Diploid organisms may be
homozygous or heterozygous for allelic forms. A diallelic
or biallelic polymorphism has two forms. A triallelic
polymorphism has three forms.
10   A single nucleotide polymorphism occurs at a
polymorphic site occupied by a single nucleotide, which is
the site of variation between allelic sequences. -The site
is usually preceded by and followed by highly conserved
sequences of the allele (e.g., sequences that vary in less
15   than 1/100 or 1/1000 members of the populations).
A single nucleotide polymorphism usually arises due to
substitution of one nucleotide for another at the
polymorphic site. A transition is the replacement of one
purine by another purine or one pyrimidine by another
20   pyrimidine. A transversion is the replacement of a purine
by a pyrimidine or vice versa. Single nucleotide
polymorphisms can also arise from a deletion of a
nucleotide or an insertion of a nucleotide relative to a
reference allele. Typically the polymorphic site is
25   occupied by a base other than the reference base. For
example, where the reference allele contains the base "T"
at the polymorphic site, the altered allele can contain a
"C", "G" or "A" at the polymorphic site.
Hybridizations are usually performed under stringent
30   conditions, for example, at a salt concentration of no more
than 1 M and a temperature of at least 25°C. For example,
conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM
EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe
hybridizations. Equivalent conditions can be determined by
varying one or more of the parameters given as an example,
as known in the art, while maintaining a similar degree of
5 identity or similarity between the target nucleotide
sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the
material in question exists in a physical milieu distinct
from that in which it occurs in nature. For example, an
10 isolated nucleic acid of the invention may be substantially
isolated with respect to the complex cellular milieu in
which it naturally occurs. In some instances, the isolated
material will form part of a composition (for example, a
crude extract containing other substances), buffer system
15 or reagent mix. In other circumstance, the material may be
purified to essential homogeneity, for example as
determined by PAGE or column chromatography such as HPLC.
Preferably, an isolated nucleic acid comprises at least
about 50, 80 or 90 percent (on a molar basis) of all
20 macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in
the Table. The first column of the Table lists the names
assigned to the fragments in which the polymorphisms occur.
25 The fragments are all human genomic fragments. The
sequence of one allelic form of each of the fragments
(arbitrarily referred to as the prototypical or reference
form) has been previously published. These sequences are
listed at http://www-genome.wi.mit.edu/ (all STS's
30 (sequence tag sites)); http://shgc.stanford.edu (Stanford
STS's); and http://ww.tigr.org/ (TIGR STS's). The Web
sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are
expressed sequence tags, and some are random genomic
fragments. All information in the websites concerning the
fragments listed in the Table is incorporated by reference
5   in its entirety for all purposes.
        The second column lists the position in the fragment in
which a polymorphic site has been found. Positions are
numbered consecutively with the first base of the fragment
sequence as listed in one of the above databases being
10   assigned the number one. The third column lists the base
occupying the polymorphic site in the sequence in the data
base. This base is arbitrarily designated the reference or
prototypical form, but it is not necessarily the most
frequently occurring form. The fourth column in the Table
15   lists the alternative base(s) at the polymorphic site. The
fifth column of the Table lists a 5' (upstream or forward)
primer that hybridizes with the 5' end of the DNA sequence
to be amplified. The sixth column of the Table lists a 3'
(downstream or reverse) primer that hybridizes with the
20   complement of the 3' end of the sequence to be amplified.
The seventh column of the Table lists a number of bases of
sequence on either side of the polymorphic site in each
fragment. The indicated sequences can be either DNA or
RNA. In the latter, the T's shown in the Table are
25   replaced by U's. The base occupying the polymorphic site
is indicated in EUPAC-IUB ambiguity code.

    II.   Analysis of Polymorphisms
        A.   Preparation of Samples
        Polymorphisms are detected in a target nucleic acid
30   from an individual being analyzed. For assay of genomic
DNA, virtually any biological sample (other than pure red
blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For

5   example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. *See generally PCR Technology:*

10 *Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila *et al.,* *Nucleic Acids Res.* 19, 4967 (1991); Eckert *et al.,* PCR

15 *Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson *et al.,* IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren *et al., Science* 241, 1077 (1988),

20 transcription amplification (Kwoh *et al., Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli *et al., Proc. Nat. Acad. Sci. USA,* 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification

25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30   B. Detection of Polymorphisms in Target DNA
There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is
carried out to identify polymorphic sites not previously
characterized (i.e., to identify new polymorphisms). This
analysis compares target sequences in different individuals
5 to identify points of variation, i.e., polymorphic sites.
By analyzing groups of individuals representing the
greatest ethnic diversity among humans and greatest breed
and species variety in plants and animals, patterns
characteristic of the most common alleles/haplotypes of the
10 locus can be identified, and the frequencies of such
alleles/haplotypes in the population can be determined.
Additional allelic frequencies can be determined for
subpopulations characterized by criteria such as geography,
race, or gender. The de novo identification of
15 polymorphisms of the invention is described in the Examples
section. The second type of analysis determines which
form(s) of a characterized (known) polymorphism are present
in individuals under test. There are a variety of suitable
procedures, which are discussed in turn.

20   1. Allele-Specific Probes
       The design and use of allele-specific probes for
analyzing polymorphisms is described by e.g., Saiki et al.,
Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki,
WO 89/11548. Allele-specific probes can be designed that
25 hybridize to a segment of target DNA from one individual
but do not hybridize to the corresponding segment from
another individual due to the presence of different
polymorphic forms in the respective segments from the two
individuals. Hybridization conditions should be
30 sufficiently stringent that there is a significant
difference in hybridization intensity between alleles, and
preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are
designed to hybridize to a segment of target DNA such that
the polymorphic site aligns with a central position (e.g.,
in a 15-mer at the 7 position; in a 16-mer, at either the 8

5   or 9 position) of the probe. This design of probe achieves
good discrimination in hybridization between different
allelic forms.

     Allele-specific probes are often used in pairs, one
member of a pair showing a perfect match to a reference

10   form of a target sequence and the other member showing a
perfect match to a variant form. Several pairs of probes
can then be immobilized on the same support for
simultaneous analysis of multiple polymorphisms within the
same target sequence.

15   2.   Tiling Arrays
     The polymorphisms can also be identified by
hybridization to nucleic acid arrays, some examples of
which are described in WO 95/11995. One form of such
arrays is described in the Examples section in connection

20   with de novo identification of polymorphisms. The same
array or a different array can be used for analysis of
characterized polymorphisms. WO 95/11995 also describes
subarrays that are optimized for detection of a variant
form of a precharacterized polymorphism. Such a subarray

25   contains probes designed to be complementary to a second
reference sequence, which is an allelic variant of the
first reference sequence. The second group of probes is
designed by the same principles as described in the
Examples, except that the probes exhibit complementarity to

30   the second reference sequence. The inclusion of a second
group (or further groups) can be particularly useful for
analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

    3.   Allele-Specific Primers

5   An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in

10   conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows

15   a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of

20   the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

    4.   Direct-Sequencing

     The direct analysis of the sequence of polymorphisms of

25   the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press,

30   1988)).

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5.   Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6.   Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita *et al.*, *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A.   Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. *See*
5   *generally* National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard *et al.*, National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by
chance.

   p(ID) is the probability that two random individuals
have the same polymorphic or allelic form at a given

5 polymorphic site. In biallelic loci, four genotypes are
possible: AA, AB, BA, and BB. If alleles A and B occur in
a haploid genome of the organism with frequencies x and y,
the probability of each genotype in a diploid organism is
(see WO 95/12607):

10 Homozygote: $p(AA) = x^2$
Homozygote: $p(BB) = y^2 = (1-x)^2$
Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

   The probability of identity at one locus (i.e, the

15 probability that two individuals, picked at random from a
population will have identical polymorphic forms at a given
locus) is given by the equation:
$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2$.

   These calculations can be extended for any number of

20 polymorphic forms at a given locus. For example, the
probability of identity p(ID) for a 3-allele system where
the alleles have the frequencies in the population of x, y
and z, respectively, is equal to the sum of the squares of
the genotype frequencies:

25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

   In a locus of n alleles, the appropriate binomial
expansion is used to calculate p(ID) and p(exc).

   The cumulative probability of identity (cum p(ID)) for
each of multiple unlinked loci is determined by multiplying

30 the probabilities provided by each locus.

   cum p(ID) = p(ID1)p(ID2)p(ID3).... p(IDn)

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

cum p(nonID) = 1-cum p(ID).

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

B.   Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(exc) = xy(1-xy)$$

where x and y are the population frequencies of alleles A
and B of a biallelic polymorphic site.

(At a triallelic site $p(exc) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)))$, where x, y and z and the
respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(non-exc) = 1-p(exc)$$

The cumulative probability of non-exclusion
(representing the value obtained when n loci are used) is
thus:

$$cum\ p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3)....p(non-excn)$$

The cumulative probability of exclusion for n loci
(representing the probability that a random male will be
excluded)

$$cum\ p(exc) = 1 - cum\ p(non-exc).$$

If several polymorphic loci are included in the
analysis, the cumulative probability of exclusion of a
random male is very high. This probability can be taken
into account in assessing the liability of a putative
father whose polymorphic marker set matches the child's
polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits
The polymorphisms of the invention may contribute to
the phenotype of an organism in different ways. Some
polymorphisms occur within a protein coding sequence and
contribute to phenotype by affecting protein structure.
The effect may be neutral, beneficial or detrimental, or
both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell
mutation confers resistance to malaria, but a homozygous
sickle cell mutation is usually lethal. Other
polymorphisms occur in noncoding regions but may exert
5 phenotypic effects indirectly via influence on replication,
transcription, and translation. A single polymorphism may
affect more than one phenotypic trait. Likewise, a single
phenotypic trait may be affected by polymorphisms in
different genes. Further, some polymorphisms predispose an
10 individual to a distinct mutation that is causally related
to a certain phenotype.

Phenotypic traits include diseases that have known but
hitherto unmapped genetic components (e.g.,
agammaglobulimenia, diabetes insipidus, Lesch-Nyhan
15 syndrome, muscular dystrophy, Wiskott-Aldrich syndrome,
Fabry's disease, familial hypercholesterolemia, polycystic
kidney disease, hereditary spherocytosis, von Willebrand's
disease, tuberous sclerosis, hereditary hemorrhagic
telangiectasia, familial colonic polyposis, Ehlers-Danlos
20 syndrome, osteogenesis imperfecta, and acute intermittent
porphyria). Phenotypic traits also include symptoms of, or
susceptibility to, multifactorial diseases of which a
component is or may be genetic, such as autoimmune
diseases, inflammation, cancer, diseases of the nervous
25 system, and infection by pathogenic microorganisms. Some
examples of autoimmune diseases include rheumatoid
arthritis, multiple sclerosis, diabetes (insulin-dependent
and non-independent), systemic lupus erythematosus and
Graves disease. Some examples of cancers include cancers
30 of the bladder, brain, breast, colon, esophagus, kidney,
leukemia, liver, lung, oral cavity, ovary, pancreas,
prostate, skin, stomach and uterus. Phenotypic traits also
include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5   individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed-to-determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a κ-squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a

5   polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer

10 potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates

15 that this treatment regime should be followed.

     For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms

20 in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17

25 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \ldots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijknp} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy

30 record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent
environmental effect common to all records of cow n; a_n is
effect of animal n and is composed of the additive genetic
contribution of sire and dam breeding values and a
5   Mendelian sampling effect; and e_p is a random residual. It
was found that eleven of seventeen polymorphisms tested
influenced at least one production trait. Bovines having
the best polymorphic forms for milk production at these
eleven loci are used as parents for breeding the next
10 generation of the herd.

D.   Genetic Mapping of Phenotypic Traits
The previous section concerns identifying correlations
between phenotypic traits and polymorphisms that directly
or indirectly contribute to those traits. The present
15 section describes identification of a physical linkage
between a genetic locus associated with a trait of interest
and polymorphic markers that are not associated with the
trait, but are in physical proximity with the genetic locus
responsible for the trait and co-segregate with it. Such
20 analysis is useful for mapping a genetic locus associated
with a phenotypic trait to a chromosomal position, and
thereby cloning gene(s) responsible for the trait. *See*
Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357
(1986); Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 84,
25 2363-2367 (1987); Donis-Keller *et al.*, *Cell* 51, 319-337
(1987); Lander *et al.*, *Genetics* 121, 185-199 (1989)).
Genes localized by linkage can be cloned by a process known
as directional cloning. *See* Wainwright, *Med. J. Australia*
159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30 (1992).
Linkage studies are typically performed on members of a
family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a
set of polymorphic markers. The distribution of
polymorphic markers in an informative meiosis is then
analyzed to determine which polymorphic markers co-
5   segregate with a phenotypic trait. *See, e.g.*, Kerem *et
al.*, *Science* 245, 1073-1080 (1989); Monaco *et al.*, *Nature*
316, 842 (1985); Yamoka *et al.*, *Neurology* 40, 222-226
(1990); Rossiter *et al.*, *FASEB Journal* 5, 21-27 (1991).
        Linkage is analyzed by calculation of LOD (log of the
10   odds) values. A lod value is the relative likelihood of
obtaining observed segregation data for a marker and a
genetic locus when the two are located at a recombination
fraction θ, versus the situation in which the two are not
linked, and thus segregating independently (Thompson &
15   Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders
Company, Philadelphia, 1991); Strachan, "Mapping the human
genome" in *The Human Genome* (BIOS Scientific Publishers
Ltd, Oxford), Chapter 4). A series of likelihood ratios
are calculated at various recombination fractions (θ),
20   ranging from θ = 0.0 (coincident loci) to θ = 0.50
(unlinked). Thus, the likelihood at a given value of θ is:
probability of data if loci linked at θ to probability of
data if loci unlinked. The computed likelihoods are
usually expressed as the $\log_{10}$ of this ratio (i.e., a lod
25   score). For example, a lod score of 3 indicates 1000:1
odds against an apparent observed linkage being a
coincidence. The use of logarithms allows data collected
from different families to be combined by simple addition.
Computer programs are available for the calculation of lod
30   scores for differing values of θ (e.g., LIPED, MLINK
(Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446
(1984)). For any particular lod score, a recombination
fraction may be determined from mathematical tables. *See*

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Smith *et al.*, *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5   of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV.   Modified Polypeptides and Gene Sequences
20   The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown
in the Table.

Variant genes can be expressed in an expression vector
in which a variant gene is operably linked to a native or
5   other promoter. Usually, the promoter is a eukaryotic
promoter for expression in a mammalian cell. The
transcription regulation sequences typically include a
heterologous promoter and optionally an enhancer which is
recognized by the host. The selection of an appropriate
10   promoter, for example trp, lac, phage promoters, glycolytic
enzyme promoters and tRNA promoters, depends on the host
selected. Commercially available expression vectors can be
used. Vectors can include host-recognized replication
systems, amplifiable genes, selectable markers, host
15   sequences useful for insertion into the host genome, and
the like.

The means of introducing the expression construct into
a host cell varies depending upon the particular
construction and the target host. Suitable means include
20   fusion, conjugation, transfection, transduction,
electroporation or injection, as described in Sambrook,
supra. A wide variety of host cells can be employed for
expression of the variant gene, both prokaryotic and
eukaryotic. Suitable host cells include bacteria such as
25   *E. coli*, yeast, filamentous fungi, insect cells, mammalian
cells, typically immortalized, *e.g.*, mouse, CHO, human and
monkey cell lines and derivatives thereof. Preferred host
cells are able to process the variant gene product to
produce an appropriate mature polypeptide. Processing
30   includes glycosylation, ubiquitination, disulfide bond
formation, general post-translational modification, and the
like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, *i.e.*, 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5   *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is

10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene

15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. *See* Hogan *et al.*, "Manipulating

20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. *See* Capecchi, *Science* 244, 1288-1292

25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active
fragments include any portion of the full-length
polypeptide which confers a biological function on the
variant gene product, including ligand binding, and
5   antibody binding. Ligand binding includes binding by
nucleic acids, proteins or polypeptides, small biologically
active molecules, or large cellular structures.
      Polyclonal and/or monoclonal antibodies that
specifically bind to variant gene products but not to
10   corresponding prototypical gene products are also provided.
Antibodies can be made by injecting mice or other animals
with the variant gene product or synthetic peptide
fragments thereof. Monoclonal antibodies are screened as
are described, for example, in Harlow & Lane, *Antibodies, A*
15   *Laboratory Manual*, Cold Spring Harbor Press, New York
(1988); Goding, *Monoclonal antibodies, Principles and*
Practice (2d ed.) Academic Press, New York (1986).
Monoclonal antibodies are tested for specific
immunoreactivity with a variant gene product and lack of
20   immunoreactivity to the corresponding prototypical gene
product. These antibodies are useful in diagnostic assays
for detection of the variant form, or as an active
ingredient in a pharmaceutical composition.

      V.   Kits
25   The invention further provides kits comprising at least
one allele-specific oligonucleotide as described above.
Often, the kits contain one or more pairs of allele-
specific oligonucleotides hybridizing to different forms of
a polymorphism. In some kits, the allele-specific
30   oligonucleotides are provided immobilized to a substrate.
For example, the same substrate can comprise allele-
specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.
Optional additional components of the kit include, for
example, restriction enzymes, reverse-transcriptase or
polymerase, the substrate nucleoside triphosphates, means
5   used to label (for example, an avidin-enzyme conjugate and
enzyme substrate and chromogen if the label is biotin), and
the appropriate buffers for reverse transcription, PCR, or
hybridization reactions. Usually, the kit also contains
instructions for carrying out the methods.
10   The following Examples are offered for the purpose of
illustrating the present invention and are not to be
construed to limit the scope of this invention. The
teachings of all references cited herein are hereby
incorporated herein by reference.

15   EXAMPLES
         The polymorphisms shown in the Table were identified by
resequencing of target sequences from three to ten
unrelated individuals of diverse ethnic and geographic
backgrounds by hybridization to probes immobilized to
20   microfabricated arrays or conventional sequencing. The
strategy and principles for design and use of such arrays
are generally described in WO 95/11995. The strategy
provides arrays of probes for analysis of target sequences
showing a high degree of sequence identity to the reference
25   sequences of the fragments shown in the Table, column 1.
The reference sequences were sequence-tagged sites (STSs)
developed in the course of the Human Genome Project (see,
e.g., Science 270, 1945-1954 (1995); Nature 380, 152-154
(1996)). Most STS's ranged from 100 bp to 300 bp in size.
30   A typical probe array used in this analysis has two
groups of four sets of probes that respectively tile both
strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.
5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three
10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in
15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included
20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or
25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of lable bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For
30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the
nucleotide occupying the interrogation position of the
probe showing the highest intensity (see WO 95/11995). The
existence of a polymorphism is also manifested by

5   differences in normalized hybridization intensities of
probes flanking the polymorphism when the probes hybridized
to corresponding targets from different individuals. For
example, relative loss of hybridization intensity in a
"footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a
polymorphism) (see EP 717,113). Additionally,
hybridization intensities for corresponding targets from
different individuals can be classified into groups or
clusters suggested by the data, not defined a priori, such

15 that isolates in a give cluster tend to be similar and
isolates in different clusters tend to be dissimilar.
Hybridizations to samples from different individuals were
performed separately. The Table summarizes the data
obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.
        From the foregoing, it is apparent that the invention
includes a number of general uses that can be expressed
concisely as follows. The invention provides for the use
of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer,
inflammation, heart disease, diseases of the CNS, and
susceptibility to infection by microorganisms. The
invention further provides for the use of any of the
nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The
invention further provides for the use of any of the DNA
segments as a pharmaceutical.

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All publications and patent applications cited above
are incorporated by reference in their entirety for all
purposes to the same extent as if each individual
publication or patent application were specifically and
5   individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C	T	---	⋮	TGTGAAACTCCACTTGAAGCCAAAGAAGAAACTCACACTTAAAAACACATGCCAGTTGGGAAGGTCTGAAAACTCAGTGCCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTGTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTGAGGATAAATGTTACTAGACTTTATGCCATGGTGCTTT[C/T]AGTTTAATGCTGTGTCTCTGTCAG
WI-10744	61	G	C	---	⋮	AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGAGGAC[G/C]AAAAACACTCTTCTGTGCGGATATCTGTGCAGATAGACCCAAAGATGCTACCCAGATGTGTTTTGATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAAGAAACTGAGACAGATAATTCTGAATTAAATGAGGTAAAGTTTCAGGCACTCA
WI-9975	126	C	T	---	⋮	GGGCAAATTACCAGCAAAAAGTCAAATACCAGCATCAAAGTCAGGTGCAAAGGAGGTAGAACAATTACAGTAACTATGTCAATCTTTTGTTATATTAGTATTATCTGCCCAATGCCTAGAATA[C/T]AGTGGGTCCCTAATAGTTATTAGTTCCTTTTCTCCTCTTCTCTGAATTTATTTTTATACTTAAGGGATTAGTTACCACCAAAAAATGTGTATGTATCAATTGATTCTTACTGAA
WI-8010	247	G	T	---	⋮	GCTAGGTTTGTTTCTGTGGCTGTCTTCACTAGACTTGAGATGACTTGAGAAGTAATCCCTATGTGATGTAACTAGTCTAGACCTTCCCTCTCCGCAATTCCCAGCTCCAGGTTTCAGAAGTATGCCACACTCAACCCTTCTCTCCAGTTCATCCTGTATTAATTTCTTCCCATATTAATTCAAAGGGAGGTGGACAGGTCCCTGGCTGAAAAGAAATAAAAGAGATCCCCAAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G	C	---	⋮	GCCCGGCCTATCTTTAATTTAACTGTATCTTTGGTGTTTCTCCATCCTA[G/C]GATTCTGCCTTATAATCTTTGTCCTGTCTGTAGATTACCTGATTCTACTTTTCTCTGCTATTGAGGACATTCCACTTTGTCACAATGTAGTAGTGCCAATTCTTCAGGTCTCTTCTTGAATTTTCTCTGCTATTGAGGACATTCCACTTTGTCACTTATCTCGACTCTATAACAACTCCAACAGAA
WI-5222	52	G	C	---	⋮	GCCCGGCCTATCTTTAATTTAACTGTATCTTGGTGTTTCTCCATCCTAGGATTCTGCCTTAT[G/C]ATTACCTGATTCTACTTTTCTCTGCTATTGAGGACATTCCACTTTGTCACAATGTAGTAGTGCCAATTCTTCAGGTCTCTTCTTGAATTTTCTCTGCTATTGAGGACATTCCACTTTGTCACTTATCTCGACTCTATAACAACTCCAACAGAA
WI-8007	242	C	A	---	⋮	TATGCACTTCCACAAAAGGCGATATAATTTAAAAGTTTTTCATTAGAAATAAAATGTATAAAAATAAATATGTTATTATAGGCATTTATTAACTATAGTCCTTCTTGGAAGGAACACCCAAACCAATACTTATAAAGTACATGTAATTTATAGTAACATATTTACTATATACATATGGAAAAAATCATATTCTCACAGAAGAGCTGAACAGACATTCACCAGGATACGACTGTTGGAC[C/A]AGCTGCTG
WI-9823	97	C	T	---	⋮	TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTCTGTGCATAAACATGTGTGTTTTGTTAGTCTATATTCAACATGAGTGAAATTTC[C/T]GGGGCATGGAAATACATCTTTATGAGACATTGAACTGCTCACCACTATCATGATCCATTAAAGACAGACCAACAATGTATAAGAATTCCCTTTGTTTTACATGCTTTCCAATCTGATTTGTATGACTATTGGATCACC

ID	Pos.	Allele	Allele	Sequence
WI-9651b	105	A	T	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGATCCTCCTCCTGGAATTCCTTTCCTACTTGTCCTCCATGTACAATTTCTGCTCGTCCTTCA[A/T]GGGGCAGCTTGCAAGCCTCCCTTTAGACACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCTTATAGGCCTCTGTCTTTAAACCTGTAATGGTATATTAAATCCTTGGTGTTTGAATGTCTCTC
WI-9651	139	T	C	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGATCCTCCTCCTGGAATTCCTTTCCTACTTGTCCTCCATGTACAATTTCTGCTCGTCCTTCAAGGGGCAGCTTGCAAGCCTCCCTTTAGACACCTC[T/C]ACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCTTATAGGCCTCTGTCTTTAAACCTGTAATGGTATATTAAATCCTTGGTGTTTGAATGTCTCTC
WI-7676b	309	A	C	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTCGTGGGACTTGGCCCTGCTATTATTTTTGTATTTATGTCTTAATCTCTTCCCACTGATGCATCCTCCAAGGGTAGATGGGGAGGGTCTGTGTGAAGGGGCCGGGCTTCTTCTTGGTGCCTGCTCGGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTCGCTGGTGCTCCCCCGTCTCTCCTGGAGGCAGTATAGGAGAGAGAGAAGGATT
WI-7676	139	C	T	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTCGTGGGACTTGGCCCTGCTATTATTTTTGTATTTATGTCTTAATCTCTTCCCACTGATGCTGCTGGGTGCCTGCTCGGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTCGCTGGC[C/T]GGGCTTCTTCTTGGTGCCTGCTCGGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTCGCTGGTGCTCCCCCGTCTCTCCTGGAGGCAGTATAGGAGAGAGAGAAGGATT
WI-10072	105	G	A	CATTATCTTGTCCTGGGTCGTGTTCATTCACTTCCTCTCTCCAATGAAGAGGATATTTAAGCATCATTCATCTGGCCCTTTTTGAATATTTTTGT[G/A]TGACTCCTATGCACATGTAAATTTGTTATGCTTGTCTTCTTATCTTTTGTTGTATAGGAGTTTTGGCCATGACCCTTTATGAGGAGAAAAGGGATCACCCCCTTTTTGCCTCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	T	C	TTGGTGTGAACTCAGAATCAGGGAAAATAAGACAATTTGAA[T/A,C]GTACCCCAGGAAACAAGAGCCCTGCACTTGACTCCAAAAGGAGTTCTATTATTCTGGCTGTTTCCAGACTTATTGTATCTTGAGAAGAGAACTGTTTTCCCTCTAAATCAGTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCAATATCAATAGCATATGGGGTGTTGGATTCTTAGAACTTATTGCAATT
WI-7041	174	C	A	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGAGGGCCTGCACATGCAAACTCCAGTCCCTTGCCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTTATTTCAGGGCTTTGCATGCGCTCTATTCCCCCTCTGCCCTCTC[C/A]CCACCTTCTTTGGAGCAAGGAGATGCAGCTGTATTGTGTAACAAGCTCATTGTAACAGTGTCGTTCATGTAATAA
WI-7224	134	T	C	ATAAACCCTTGTGTATGTATCACCCAACCTCACTAATTATCAACTTATGTGCTATCAGATATCCTCTACCCTCACGTTATTTTGAAGAAATCCTAAAACATCAAATACTTTCATCCATAAAAATGTCAGCATT[T/C]ATTAAAAAACAATAACTTTTAAAGAAAACATAAGGACACATTTTCAAATTAATAAAAATAAAGGCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGTTCATGCTAG

ID	Pos			Sequence
WI-10826	132	A	C	TCTTTATTTGCATTCACAGTAGCCCCATGAAGTAGGTATAACCAGCCTCTATTTAACATGAGAAGAT GGAGGCCTTTTCCAAATGACTAAGTAATGTGTCTCAGGTTTTCTCAGGTTTTTCTCAATAAGCAAAGACCTGCA[A/C] CCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCTGTGCTGTCAGCCAGGACCCCATGCGGCA GAAAGCCCAGCCTCCTCCATCCCCCAC
TIGR-A004S25	145	G	A	AGATCTGCCATTAGTATTATTCCTTTGAAGATACTTTGGAGATTCATTTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAAACTTGTGGGGTATAGAAATGGAATGGAGAGTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGCTGTCCTGTCCTGTCCTAGGCATTGAAACCATCACCTGGTTTGCATTCTTC ATGACTGAGGTAACTTAAAAATGACTGAGGTTAACTTAAAAC
WI-1021	24	A	T	AAACACACAGAATCATCAAAGCAC[A/T]ATCTGTGTTGAGATAAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACTCTGAAATAGTAGGATAGTATTATCATTCCTGTAATAGATCCTCTCAGCAAT TGGGTCTGTTTTCATTCTATGGAAACTCTCCGTACTGTAATTTTCATTCTATGGAAACTCCCCATACTGT AATTGGACAGTTTTGGTTTCCAC
WI-4687	121	G	T	TAGTATGTCACTGCCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTTGTCC TTTCAATAAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGATTAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAAATAG GAGGCCCTGAGATCCCACTGGATAATCTAAAAAACCAAGAGAAGAAAGAAACTTGAT
WI-4719b	107	T	G	TTCATTTCCCTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT ATGTCTGACGCGCCATGGGTGTTCATAAGTGACTTGAGAGT[T/G]ACTGTAGAGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-4719	70	G	A	TTCATTTCCCTTCCAAAATCCTTAGGAAATTTACATTAAGTGACTTGAGAGGCGGATT AT[G/A]TCTGACGCCATGGGTGTTCATAAGTGACTTACTGTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAACAATTCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-9484b	216	G	C	TCAACACGCTTTATTGCCACTTCTGGCTCCGTCCCCGTCCCCGTCGTCCCGTCCCTACCCTGTAGG AATACTGAGCTCCGATGCAGGGAATGGGGGTGTTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCCTGCTTGCTGGAGAGGAGGGCCAGAGGAATTCAAGGGCCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGGACCAGGGTTCCAAACTTT
WI-9484	178	G	A	TCAACACGCTTTTATTGCCACTTCTGGCTCCGTCCCCGTCCCCGTCGTCCCGTCCCTACCCTGTAGG AATACTGAGCTCCGATGCAGGGAATGGGGGTGGGGGTGTTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCCTGCTTGCTGGAGAGGAGGGCCAGACAGG[G/A]AGGAATTCAAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGGACCAGGGTTCCAAACTTT

WI-7330	207	C T	AGGATGGAAGGAGACACGGGCAGGGAGGAGAACTCTCTTCTGTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCGCCACTGACATGGTTGGCTGGAATTTCTTCTTTAATTGTGGCATATAGGTTT GTGACACAAGAGAGTCATACTCTTGGTGGCTAAGTTTACTAAGGAAAATAACTGAAAAGATTAAAAG TGAGAG[C/T]TGAAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTCACAG
WI-9443	211	G A	TTAAAAACAGTTCAGGTTGGGTGAAGCAGAAAAGGGATGGTGATTACAATTTAAATGAATCAGTCACTT GCACAATTAATCCTCTTGGCATCATACAAACTGGGTTTAATGGCAAATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACCTGAGGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGAGATGACACACCATGCCCACTT
WI-7166	59	C T	TCTCTCAAAAGAGAAAAACAAAACCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCCTTGTGCAAAATATTGACTATTCTGTATCTTTCATCCTTGACTAAATTCGTG ATTTTCAAGCAGCATCTTCTGGTTTAAACTTGTTTTGCTGTGTGAACAATTGTGAAAAAGAGTCTTCCAAT TAATGCTTTTTTATATCTACCTGTTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C, C	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAAACCTTCAGAGAGGAGGGGGAGCAATTTTAGCC CCACCCTGCTCCCATCTGCCCCCCTGCCAACAGCTGCAGGCTGCTTCCTCTCTGAGTTCCTCTGGGCT GCGCAGGCTGCCCCTGGGAATAGAGCAAGAGACGTGAGTCCTAACCTGGCCACA[G/C,T]TGGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGCTC
WI-7259	188	G T	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAAACCTTCAGAGAGGAGGGGGAGCAATTTTAGCC CCACCCTGCTCCCATCTGCCCCCCTGCCAACAGCTGCAGGCTGCTTCCTCTCTGAGTTCCTCTGGGCT GCGCAGGCTGCCCCTGGGAATAGAGCAAGAGACGTGAGTCCTAACCTGGCCACA[G/C,T]TGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGC
WI-7322	275	A G	GTACTTTAGGCCTGTGTGGAGGGGTGGGCATTTAGTGGTGACCCCTTGCACCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTTATAGCCAGTCACATTTGCCCTCTCACCCTATATG GCCATAAACTGCCTAAGCACTCAGCCTCATCAACCCCTTTGACCAGAGAAAGAAGCACTC TGGTTCTCTATCCCCTTGTCACATAGAGAGTTTGTCATGGGGCCCTCTGGCTG
WI-7685	46	T C	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTTGGGCTC[T/C]TTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGTCTTGGAGCTGAGCCTCTCACCTGTACTCTTCCGAAAAATCCT CTTCCCTCTGAGGCTGGATCTCTAGCCTTATCCTCGATCTCCATGGCCTTCCTCCTCCGTGCCGACTC CTGGGTTGAGCGTGTTGCCTCAGTGCCCCCAACGATGCTTTTCTGTCTC
WI-563	87	G A	TGTGACCAATTGTTATTTTAGAGGGTTTAACAATGGCCTGACTATCACCTGACTGTGGTGCGCCAGAATTTC CTGGGGGGAGGGGCCTCCCCCT[G/A]CCCTGATCATCGTCTCACCTAACTGCCTACTCTAACAATACTACTCC TGTGGTATGGGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCCTCAGTAAAGGCAAATTTAAATCTCTTTGGATAACCCAGGGCACAT

Name	Pos.			Sequence
WI-931c	191	C	A	GACCAGGGCACCAGAAAGCCACGGAAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCCTCCCTATCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCATTACTGTTGTATGGATTTATAATTATTGTCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGGAAAGATGTGTCAGA
WI-931b	81	A	G	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCCTCCCT[A/G]TCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGTATGGGAAAGATGTGTCAGA TACAGAAAAGGCATGGGGAAAGATGTGTCAGA
WI-931	31	A	G	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[A/G]GCCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTTCTCTCCCCTCCCTATCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGTATGGATTTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGGAAAGATGTGTCAGA
WI-10870b	91	C	T	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-10870	103	G	A	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGGCACCTACTTAGA[G/A]CAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-7719b	281	T	C	AGTTATTCTTCCAGATGACCAGCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATATCCTCACTGATTTCAAGCTAAAGCAA
WI-7719	163	A	G	AGTTATTCTTCCAGATGACCAGCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C	A	GCCTTGGAGTAGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAAACATTGCTATCAACTGGGAA GAGT[C/A]TGTGGACTTTATGCCCAGTTTCCCCTCTCCAGATTTTTATGACGGTTGTTTTCTTTTTGTTA TGCCATTTGAGGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTCAGG TTAAACAGCCACCATTTGTAAACACTTTGT

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WI-10673	94	C	G	--	TCCCTTTATGCACCCAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACCCACCCCCGTGGCACTCATGGAGGGGG[C/G]TGCAGGTTGGAACTATGCAGTGTGCTCCGGCCACACATCCTGCTGGGCCCCCTACCCTGCCCCAATTCAATCCTGCCAATAAATCCTGTCTTATTTGTTCATCCTGGAGAATTGAAGGGAGGTCAAGTTGTTGTCAATGATTTGTCAGAGAACCT
WI-7842	57	T	C	--	CACAGCCATGCCCTTGAGGAGACGCGGCCACCAGATGCTGAATCCCTATCCCATTCTGT[T/C]GTATGAGTCCCATTTGCCTTGCAATTAGCATTCGTCTGTCTCCCCAAAAAGAATGTGCTATGAAGCTTTCTTTCCTACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAATTCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTCAGCTCCCTATA
WI-7721	145	A	C	--	CTGCCTCATCACGCCACTGGAGTCCACACTTGAATTTGGGCAGTCACCAGGGTCTGCCATGCTCTGGAGGAGCAAGGGGCCACATCCCACCCCACCCCAGCTGTTACCCAGCCCGGGCAGGTGCAGCCCTTCCTCCCTGTCTCTGC[A/C]TCGACTCTCTTTGAGGTCCCTGTATGTCACCTCTGACTTCTGTGGTCCCTCTGTGTCTGCTCATCCATTCCTCTTACTGGGCCTGGGGCCTCTAGCCCAA
WI-4767b	173	C	A	--	TTTCCAGTCTGTTTATCCTTTCATTGTCAAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTTCCTCAGGTCTCGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGAGGGTATGTTTCTTGCCTTGAGAAATCCTAGAAAGCACAGGGATGACAAATCACTAAGGAATTCCACTAAGACCTCCTCTAACCCAGAGATTTTTAACCT
WI-4767	50	A	G	--	TTTCCAGTCTGTTTATCCTTTCATTGTCAAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTTCCTCAGGTCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTGAGGGTATGTTTCTTGCCTTGAGAAATCCTAGAAAGCACAGGGATGACAAATCACTAAGGAATTCCACTAAGACTCCTCTAACCCAGAGATTTTTAACCT
WI-7718f	222	C	T	--	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTACTCCCTACACTGATGCAAGGATTACAGAAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAGAGGTGAAAGGTGAAAGGAGCTGTGTTGAAACAGAAAATAAGTCAAAAGGAACAAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAT
WI-7718e	60	T	C	--	ATTGCACTGAAGTTTTTGAAATACCTTTGTGAGTTACTCAAGCAGTTACTCCTACACTGA[T/C]CAAGGATTACAGAAAACTGTGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAATAAGTCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718d	31	G	A	--	ATTGCACTGAAGTTTTGAAATACCTTTGTA[G/A]TTACTCAAGCAGTTACTCCCTACACTGATGCAAGGATTACAGAAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAGAAATGAAGAAGGAAGCTGTGTTGTTGAAACAGAAAAATAAGTCAAAAGGAACAAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT

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WI-7718c	91	C G	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGG[C/G]GAGTGAGTTCAACTACACATGTTCTGGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAGAAAAACTATGTATTAAT
WI-7718b	248	A G (C)	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACATGTTCTGGGGGCCCGGAGATAG ACTTTGCAGATGGAAAGAGGTGAAAATGAAGAACAGAAAAATAAGTCAAA AGGAACAAAAAT[A/G]ACAAAGAACCATGCGAGGAAGGAGAAAAACTATT[A/G]AT
WI-7718a	42	A T	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C,T]GTTACTCCCTACACTGATGC AAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACATGTTCTGGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAGAAAAACTATGTATTA
WI-7227d	99	G C	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAAGCTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G A	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAAGCTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAGAGGGACTGAGCTAAACAGTG TTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93	G T	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAA[G/T]CTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A G	AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGC TTCCGTGGACCAATTCATCTTTCAGACACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234	A C	CCACAATGCCTCTCCCACGATGTCAAGGACTCCTGTCTGTCGTGGGGAGCAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAAACTGATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGGACATGTGCTATTGAACTGAGCCAAACACTGTAAAT ATCCACAGACTCCCTCCCCTGCCCATCCCA[A/C]ATGATCTTGAGATTTC

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WI-7310a	64	T	A	---	CCACAATGCCTCTCCCACGATGTCAAGGAGGACTCCTGCTGTCTGTCGTCCTGGAGGTGGGAGACAAGGAACC[T/A]CCGAAGAGAGAAGCAAGAAAGCCGTACTGTCTATGTTGTGACTCATCGAAACTGATGCGAAAACTTGAATCTGTTACTGAAATGAGGAGAAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAATATCCACAGACTCCCTCCCTGCCCCCAAATGATCTTGAGATTTC
WI-7878b	162	A	G	---	CCAGCAACACCTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCAGATCATGCCCAAGACGGGCCTCCTGATAATCGTCTTGGGCATGCAATGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGGAGCTG[A/G]GTGGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
WI-7878a	51	C	G	---	CCAGCAACACCTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTG[C/G]TGGTTGATAATAATCAGATCATGCCCAAGACGGGCCTCCTGATAATCGTCTTGGGCATGCAATGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGGAGCTGAGTGGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
WI-7381c	213	C	T	---	CTCCACATTCCCACAGGCCTTGAGACTGAAGGGAAATCCCCCTTTCTTTCTACCAGCCCTGCAAGTTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACAAAACGGCCTC[C/T]GGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54	C	G	---	CTCCACATTCCCACAGGCCTTGAGACTGAAGGGAAATCC[C/G]CCTTTCTTTCTACCAGCCCTGCAAGTTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53	C	G	---	CTCCACATTCCCACAGGCCTTGAGACTGAAGGGAAATCC[C/G]CCTTTCTTTCTACCAGCCCTGCAAGTTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93	G	A	---	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAAG[G/A]GATGTAGATTGTCACATTCAATCCTGAAACAAACCTGCCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCACTGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC
WI-1017a	92	G	A	---	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAAAATTGAACTCTCTGAGGTACTGACTGTGGGACCAGCAGACAAG[G/A]GATGTAGATTGTCACATTCAATCCTGAAACAAACCTGCCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCACTGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC

WI-1795b	130	T	C	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTGTCTGGGTTCTTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAAGAAAAGT[T/C]C GTCTACCATTTTCACCAAATTTCGTAGTACAATTTAAGTATCTCTGTTATCTCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGGATTT
WI-1795a	47	T	C	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGT[T/C]CTTCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAAGAAAAGTC GTCTACCATTTTCACCAAATTTCGTAGTACAATTTAAGTATCTCTGTTATCTCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGGATTT
WI-10616d	136	G	A	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCCTATCACATTGCCA C[G/A]TAGCCCTCCCTTCCCCTCACAGGCCCTTCTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616c	136	G	A	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCCTATCACATTGCCA C[G/A]TAGCCCTCCCTTCCCCTCACAGGCCCTTCTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616b	141	C	T	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCCTATCACATTGCCA CGTAGC[C/T]CTCCCTTCCCCTCACAGGCCCTTCTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616a	116	G	C	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTG[G/C]TCTCCTATCACATTG CCACGTAGCCCTCCCTTCCCCTCACAGGCCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-1126c	52	G	A	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTTCCAGTATCACT[G/A]ATACTAATATAA AAACCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGCAAGAA AATTTATTTCTCAAGATATAAAAAATAAAATATTTAATTCAGTTTCCTCAAAAGGAATATGAAATT TGTTAAAATGCAAATCCAGCTGTAACTTTTTGGACTGTCTTTTATTTCTT
WI-1126b	230	T	C	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTTCCAGTATCACTGATACTAATATAAAAA CCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGCAAAGAAAATT TTATTTCTCAAGATATAAAAAATAAAATATTTAATTCAGTTTCCTCAAAAGGAATATGAAATTTGTT AAAATGCAAATCCAGCTGTAAC[T/C]GACTGTCTTTTATTTCTT

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WI-1126a	97	T	C	CTCTTATTTCTTCTGGGCACTGCTTCTTCTGGGGGCAAACTTCCAGTATCCAGTATCACTGATACTAATATAAAAA CCCTGTGAAGTGCTGCTGCATTTCAAGAT[T/C]CAATATATATATCCAGATTGTTTCCCAGCAAGAGAA AATTTTATTTCTCAAGAGATATAAAAAATAAATATATTTAATTCAGTTCCTCAAAAGGAATATGAAATTT GTTAAAATGCAAATCCAGCTGTAACTTTTTGGACTTGTCTTTATTTCTT
WI-11183c	124	C	T	TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGT[C/T]ACTAACATT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192	T	C	TAGTGCTAATTTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGC[C/T]CTTGTCACTAACA TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTAAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118	C	T	GCTTGGTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTCTGCCTGGCCCTTGTATTCA CCCATACCTCGTCTCAGACCATTCCTCTATCTGGAGCGGCTCTTCCTTCCTG TTCACCAACCTTCTTTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCCCTTTCCC
WI-10770b	174	G	A	GCTTGGTTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTCTG[G/T]CTGGCCCTTTGTATT TCACCCATACCTCGTCTCAGACCATTTCCTCTATCTGGAGCGGCTCTTCCTTGTACTTTCTC CTGTTCACCAACCTTCTTTTTATTCTTCAGGACACTCAGTTGTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCCCTTTCCC
WI-10770a	49	G	T	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTGTATCATGG TTATCACTGGACA[C/T]AGCCACCACCTCCCCAGGCTTAGAACTCCATGAGTAAGGGACCCTGTCTA ATGTGCCGTTCTCCTTATGGTATTACACACAGTACCTAAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667b	82	C	T	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTGTATCATG[G/C]TTATCACTGGACA[C/T]AGCCACCACCTCCCCAGGCTTAGAACTCCATGAGTAAGGGACCCTGTCTA ATGTGCCGTTCTCCTTATGGTATTACACACAGTACCTAAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68	G	C	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTGTATCATG[G/C]TTATCACTGGACACCAGCACAGTACCTAAGTCAACTAATGGATCTTGGCT ATGTGCCGTTCTCCTTATGGTATTACACACAGTACCTAAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

Name	Position			Sequence
WI-10400d	189	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTCAGAGACATCTGCTG GTTAAC[G]TTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTAATTTT TCTTTCCCTTACCTTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCCATGTAG
WI-10400c	166	A	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTCAGAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACTACTAACACAATATTTATTCTAATTTT TCTTTCCCTTACCTTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400b	165	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTCAGAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACTACTAACACAATATTTATTCTAATTTT TCTTTCCCTTACCTTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400a	46	T	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATAAATAGAAAGTAA[T/C]TGCATTTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTA ATTTTTCTTTCCCTTACCTTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78	C	T	AAAGGGCTACAAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGGTAAATGCAAGGGGAGACCC CACCTCTCACCA[C/T]TAGAAAAGGGCATTCAAGCACCATTCAATGAGGCTTCATATACTGGTTAG CAAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAGTGATGAGGCCACA GTGAATATCCACCTAAGCGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33	C	T	AAAGGGCTACAAACTAAGGCCAAAAACCATGAA[C/T]GGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCATTAGAAAAGGGCATTCAAGCACCATTCAATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAGTGATGAGGCCACAG TGAATATCCACCTAAGCGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266	T	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCCTGCCACATCCAGCTTGTTGTCC CAATGAAATACTGAGATGCTGGGCGTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCCCAGGGCCCAGAC AAGAAGACTGTCAGGAAGGGTCGGGAGTTGGCTTTTTTCACATTGAT CATTTTATATGAAATAAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140	A	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCCTGCCACATCCAGCTTGTTGTCC CAATGAAATACTGAGATGCTGGGCGTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCCCAGGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGGAGTCTGTAAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA

ID	Pos	Alleles	Sequence
WI-7038a	31	G A	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTTCCCTGCCACATCCAGCTTGTTG TCCCAATGAAATACTGAGATGCTGGGCGTGTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGTCGGAGGTCGTGAGTCGTGTAAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAAGATCCTGCATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	ATACGCTTTCTGTCTGTCCCACAGTGGAACCAGCACCAGGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCCTCAGCGCCCTCAGCTTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGAACCAAGCACGGAGC
WI-3429a	62	C T	ATACGCTTTCTGTCTGTCCCACAGTGGAACCAGCACCAGGTGGCCAGGGTCGGGCTCCACACA[C/T]AG CCCTCAGCGCCCTCAGCTTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGAACCAAGCACGGAGC
WI-6786c	151	G A	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGATAAAGAAGTGAGTGACGGTGACCT GTGAGCCCCATTCTTCT[G/A]TGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTGGCGAAAGGAT[A/T]AAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAA[A/T]GGATAAAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCTAAACCTTCAGTTCCAATCACTCTGAAT TTCATATACCTCCATTATTAAATTCAATACATCATTGCAGAGAAAAGACAACGGTGCCAACTGGGTT TGGTTGGTCCTGCCACACCCACA[G/T]TGGCAACTAAGTGTAATCTCTAAA
WI-6711a	36	T C	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAA[T/C]TGAATAAGTATTGGGGAAGAATCCCTA CCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCTAAACCTTCAGTTCCAATCACTCT GAATTTCATATACCTCCATTATTAAATTCAATACATCATTGCAGAGAAAAGACAACGGTGCCAACTG GGTTTGGTTGGTCCTGCCACACCCACA

WI-10613b	172	A	C	ATTGTGTATGCCAAAATCATAATACCCTGCATTCTAGAAACATACAGTGTAATAAGATGTAAATAGAATTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACTACGTTTAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTG[A/C]GCCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G	A	ATTGTATGCCAAAATCATAATACCCTGCATTCTAGAAACATACA[G/A]TGTAATAGAATTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACTACGTTTAACATCAATGAATGTG ATTTTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A	T	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAGATCTGTGCTTCCAACAAGTGACTACCCTTGAAGC ACATCCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGGCGTCTTTTCCAGCCCCTGAGGAAA T]GGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCCTCT TCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587b	81	G	A	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAGATCTGTGCTTCCAACAAGTGACTACCCTTGAAGC ACATCCCCTTCTG[G/A]ATCTGAAAAGAGCCCTTGGCTCAGGGGCGTCTTTTCCAGCCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCCTCTT TCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587a	28	C	T	GCTCTAGTGGGAAACCTCAGGTAGCTCC[C/T]GAGATCTGTGCTTCCAACAAGTGACTACCCTTGA AGCACATCCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGGCGTCTTTTCCAGCCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCCTCTT TCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-10681b	103	T	A	ATGACTCAGGTGACAAAAGAAGGAAGCATGTCCTAGACCCCATTGACTTACGGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTTAAAAAAGCC[T/A]AAAGACAGCCATTTTAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTCCCCACACAGAAAGAAACTTCAAGGTTCTAAGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGGAAGGAGGAGGTGACGCTCTGTTAAAAG
WI-10681a	41	A	T	ATGACTCAGGTGACAAAAGAAGCATGTCCTAGACCCCATTG[A/T]CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTTAAAAAAGCCTAAAGACAGCCATTTTAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTCCCCACACAGAAAGAAACTTCAAGGTTCTAAGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGGAAGGAGGAGGTGACGCTCTGTTAAAAG
WI-7222c	126	G	T	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGGAATTCCCTTGAACAAGAGAGAAACTGGGGATAGTTATATTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTTGTGTAAGGTTGTATTCAAAGACTGAATTCATTT

ID	Position	Allele	Allele	Sequence
WI-7222b	255	G	A	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGGGGAATAAAGG AGGGGGAATTCCCTTGAACAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G	T	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGAGGGGAATTCCCTTGAACAAGAAGAAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTT
WI-8054d	41	C	A	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTT[C/A]TATCTCCTCCCAGTTCAAAATG CTTGCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTTCTTGTAGTTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054c	237	G	T	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTCTTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTGTAGTTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TGTCATAACGCCGCTTCCCTGGGCGTACAGA[G/T]AATCCTTGCCCTT
WI-8054b	148	T	C	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTCTTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTGTAGT[T/C]TTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054a	131	C	G	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTCTTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[C/G]A CAATCTTCTTGTAGTTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-10854b	152	G	T	TTCCACAAAAACTTCCCTGGGCCGGGGGTGACTAAGATGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGTCTGGTAAGTT ACGGGTGCGAGGCAACA[G/T]GGAGAGGTACGGGAATAGTTCTACTTCCTTGTTTTTATTCTTGTG TTTTAGACACACAGGGTCTGCTGTGTTG
WI-10854a	102	C	T	TTCCACAAAAACTTCCCTGGGCCGGGGGTGACTAAGATGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGTCTGGTAAGTT TATACGGGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCCTTGTTTTTATTCTTGTG TTTTAGACACACAGGGTCTGCTGTGTTG

Marker	Position	Allele 1	Allele 2	Flank 1	Flank 2	Sequence
WI-9826b	127	G	A	---		AATTTTATATGTGAAGGGTTAGCAAACTATGGCCCACAGGCCCATTCTAGCCATGCCTATTTTTGTGTGCCTGATGGCTGTTTGGTGTTTGCACGCAGTTGAGCCAGTTGACAGAGGCTGTTAT[G/A]GCCTCAAAGCCAAAAACAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAA
WI-9826	125	A	T	---		AATTTTATATGTGAAGGGTTAGCAAACTATGGCCCACAGGCCCATTCTAGCCATGCCTATTTTTGTGTGCCTGATGGCTGTTTGGTGTTTGCACGCAGTTGAGCCAGTTGACAGAGGCTGTTAT[A/T]TGGCCCTTCAAAGCCAAAAACAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAGGCAGAGAAGATCAGAAGTGTTGAA
WI-15986	60	T	G	TTTGTTTGTGTGTGGGTTTTT	TGACATTATATAAACGTAAAAGAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTTTGTTGTGTGTGGGTTTTTTTTT[T/G]TTACATTTCTTTACGTTTTATATAAATGTCAGCATTTCAA
WI-8655	29	A	G	AACTGCAAATAGGAAACCAGGAG	CCAACTGGGGCTCCC	TTCAAGTAACTGCAAATAGGAAACCAGAG[A/G]GGGAGCCCCAGGTGGGACAAATCATGGCTACCCCTCCCCAACAGAACAGGGGAGGAGGTGGCCCCTACACCCTTTAT
WI-8170b	259	G	A	---		GCACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACCAGAACCGTGTTTTAATAGCTGCTGATAAATGAAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAGCATTTGGTGGAGAGATTACAAGGTTAAGATCATGTGTCCATCCTATCAAGTGCAATCCTATCAATCAGAAATAAAAGGTAAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T	A	---		GCACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACCAGAACCGTGTTTTAATAGCTGCTGATAAATGAAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAGCATTTGGTGGAGAGATTACAAGGTTAAGATCATGTGTCCATCCTATCAAGTGCAATCCTATCAATCAGAA A[T/A]AAAGGTAAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136	C	G	CCTTTATTAAAATTGTTTTCTTGACA	GAAGAGAAATGTAATACCTGTAAAGGTAC	CAGGATTCCTTAGTCATCTTCCAATACTCCAGGTCACATGGTGAAGAGTCACCTGTTAAACACGAAATCTAACCATTAAACAAGCTTTAAAATCCTTCGGTAACTCCCTTTATTAAAATTGTTTTCTTGACAT A[C/G]AGTACCTTTACAGGTATTACATTTCTTCTTCACCGTTTACA
WI-8183	56	G	A	TGAAATAAAAACAATTTCTGTTGC	TGTGTTGAAATCAAACCTGC	AGCAGGGGTTTGAAATTGATCCCTTTATTTTACATGAAATAAAACAATTTCTGTTGC[G/A]CAGGTTTGATTTCAACACGTTGAATCTGTAAAAACCAAAGCTGTTTCTGATGCAGGACAAAATATCCCACAATATTTAAAAACTGCAAGCACCATGC
WI-14149	83	C	T	---		GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCCAAGCATGGGATTTTGCCGGAAATATTAGCGGTTAAAGGGAGC[C/T]TGAGTTGAGTCAAACACGGG
WI-8712	44	G	A,G	CACAGGGAAGAGGTAGTGGA	CAGGAAGCCTGACCATCTC	TCAACAATGACACTGTGTAACAGCACACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCCTGTTCCTTAACCAGCAGAGCCCCAGCAACCTAGAAGCGCCTCACCTAGCCTCTTAAT

Marker	Pos			Fragment 1	Fragment 2	Sequence
WI-8827	22	C	T	TCCCCTGGGAG ACTATGG	GCGATTAGGAT TTTAGTGTTCA C	GGTGTCCCCTGGGAGACTATGG[C/T]AGTGAACACTAAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTTCCTTCTTATCCACCCAGTCTCT
WI-8833	51	A	T	TCTTCCATGCC ATTCTCTG	CCTCACACATT C	CTCCGGCCTCTTAAAGCTCTCTGTGAGACTGTCTTCCATGCCATTCTCTG[A/T]TGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63	A	G	---	---	ATTTTTAGCCATGTTGGTAAAAGTTCATTTCAGTACACATGGGTAACACCCAGGCCCTTTCCC[A/G]T TATATCCAGGTATGCTACAAGTTCTTTAACTCTTATCAGAAGTTATTATTACTGTTCCTTAGAGAG GCTACCAGGCTAAAATTCACTTAGTTTGGTTTGTCTAATGTCCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21	A	G	GGGACTTAAC CTTTGGCCT	CAAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCTGGCTGTTGGCTCTGCCGTGTTTTTGGTTTCTT TCTCTTCTACTGGTCTTTCCTTTGTCTTTGCCAGCCACCTATGCTGTGT
WI-8853	79	C	T	CCCGGGCATTG AGGATA	AGTCTTCCTGA GCCTTCCAT	ACTTTTTCTTGAGCTGAGCAACCTCATCATCCTTTAGCTTCTGGTTGATAAACGCTGGTTAATCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52	A	G	---	---	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGAACAGTCATGGTCGAACA[A/G]ACAACATGCT TCGGACTTACCAAAGGGAGGAGTCGAGCTTTCCATATAAA
WI-8865a	42	T	C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGAACAGTCA[T/C]GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGGAGTCGAGCTTTCCATATAAA
WI-8895	32	A	C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAAT[A/C]CTCCCGGTCCTTGAAATTTCCATTAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93	G	C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTGTGAAATATAATAAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATATAAACATTTCTAAGTGCTCACTC TCAACTTCTGTTGTTATCTTGCCATGGTCAACAGTTCACAGTAACAAGTTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACTCCCGTCTGCGTCTCAGTCACCCAC
WI-8496b	157	A	G	---	---	TTTCATCATCAAAAGTTTTCTTTCCATAGAAGAATGGTAATGTTGTATCGAGTGCATATTCTATGGAAA ATTCATATCTCAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G	A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAAT[G/A]TTGTATCAGTGCATATTCTATGG AAAATTCATATCTCAAGTAACTAGCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A	G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCCTCCTGCGTTGTCACCCACATCCACAGAGCA GCCCTAGTGCCAGGTGCAGCCCACTGCCCACCCGGGAACAGGACCCATGCTGC

Marker	Pos	Alleles	Seq 1	Seq 2	Sequence
WI-12108	40	C T	TGGAAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTGATTACTTCTGGAAAAGGGTTAAACTCAAATATC[C/T]GAAATACTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTATTTAA
WI-5989	29	G A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAAACGTCCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCATATATAC CCCTTCATGTCCTAAAGAAGACATTTCTCTTAGAGATTTCATTTAGTGTATCTTTAAAAAAAAT CTTGTGTTAACTTGCCTCCATCTTTTCTTGGGTGAGGACACC
WI-12201	61	C T	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCCTGGAGTGTTTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGTGGTCGGGGTGTGGGGTTGCAGCCCCTCCACTGCTCGATAAAGGC
WI-12018	31	A T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTGTTTGTTTAATGATCCGAATGCTTGAGAAGAAACCTGGCCTCGCTGCCTC[A/G]GCCTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGGG
WI-15407	92	A G	CATGCCCTTTA AGGATTAAGT TT	TCTTTTCTCTT TGGTAGTGTGG	AGCATGTAAGGAGGAGCAGTTTATTTGATTGGTATATTCAGGTTTCTAACCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAG[A/G]CCACACTACCAAAAGAGAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C	GTTGAGTATTT GTTCTGTCAT AATT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGTCATAATT[T/C]CCAATATGTACCAGACCTTCCC
WI-12326	25	G A	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAGTACTTAATACATATTTCAAAC CTGTTTGCATTTCAAACAAAGTTAGCGTTTTTGTAAATCAAATTTGATAAACCCGACTAAAAAT
WI-12361	63	C T	---	---	TTAAATTCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGGAATTTCAGCATAGTGTATTAT[C/T] TGAACTAAATTTACAAAGTGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C T	CAGACACAGC ATCACACCA	GACCCTCCCGT GGGC	ATACTGGTTTAATCCATGTCAAATGTTAGTTTACAAAGGAAAGGACAAGTACCTTTGTATAGAAATAT ACAGACACAGCATCACACCA[C/T]AGGCCCCACGGGGAGAGGTCGGGGAGGAGCGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G	GGGAGGAAAA TCCAATAAAT TTTT	CATTGGGGAAT AGCTAAACCTT CTGTGTACTGGAGCCCCG	ATTTTTATATGAAGGTTTTCTGGTGAAATCTTTTAAGCAGGAGGAGGAAAATCCAATAAATTTTTTAA[A/G]AAGGTTTAGCTATTCCCCAATGCTATTTAATACAATTGAGGTTAGGACGTTAAGTCTTATCAGA
WI-11324	40	C G	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCCA[C/G]GAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCGTTCTTGTCC

ID	Pos						Sequence
WI-11352a	69	T	C	G	AGCACAGCAC ATAGTGGAAA G	GACCTCTCGTA GGACACTTAGC CACTTA	TGACACATGGTTTCTGTTTCCAGAAGAGAGAGAGAAGTCATCTACATAAGCACAGCACATAGTGGAA AG[T/C]GCTAAGTGTCCTACGAGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C	T	G	CAGCTTGGAG ATTCTGATTCA GCAC	GCCCCGCCTGA GCAC	TTAGCCCATGCTGTCATTGCAATCACCTGTGAAACCTATGAAACTATACCTGCCCAGGCTCAGCTT GGAGATTCTGATTCAG[C/T]GTGCTCAGGCGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATGCGTATAT
WI-11385	75	T	C	G	ACAGAAGACT TTCATATTCTT GTTTTT	GATTCTATTCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAGACTTCATATTCTTGTTTTTAAAAGTC TCTTCAG[T/C]AGGAAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGAATAGAATCAGC
WI-11388	88	C	A	T	TGTTTGAAATT CAAGTTAAAAT T	TGCCTTGTATC T	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAATTAAAGAATGAATGTTTG AAATTACACGTAACTAAGTTC[C/A]TATAATTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T	G	A	GGTTATGTGTT CTTGAACTTA TGTTTTGTAAA GATAAATAC	AAG	TTCTATCATTCCATTAAAATGGGCAGGTTATGTGTTCTTGAACTTAATAAAATAC[T/G]CTTTTACA AAACACGTGAATGTACTTTTCTTGTCAGAGAGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A	T	T	TTTTGTTTTTG AAATGGTGTTT ATATTCACCCA TC	T	AAAGAATAAGATGGCATTGTTCAGTTAATTTGTTTTGAAATGGTGTTTT[A/T]GATGGGTGAATA TGAAAATAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100	C	A	TCCCCACCAAC TGCCAGGGCCT TATTTG	CAGC	CTGTCAGTCTTCCCAACTAAACCGTGAGTTCCAGTATGTGTCAGCAGCCCTGCGTCTGTCGTTCTTGGTG TATTCCCATTACTGAATCCCCACCAACCAGC[C/A]CAAATAAGGCCACAAAGTAAGCTCTCC ATTTTTGTAGAATGAAT	
WI-11466	26	C	T	GTTTATTGTTA TAAAAATGAC CTACAACTT	TC	ACTTTGAGAAGGCCATTTATTTGCAG[C/T]CTTCAGTCCAAAAAAAGTCAACATTTTCAGAATTTTT TATATAAGTTGTAGGTCATTTTATAACAATAAACTTTCTATTATCTTCATTATCTCTCACATACAITT CATGTATCCTG	
WI-13364	35	A	G	...			TTTTTCTTTTGTGCTCTTTTTTTTTTTAGTAGAAGC[A/G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTTAGACAACATACCTTTCTTTGAAATGTAAAATGTCA
WI-11276	41	A	G	GGCAGCCCAGG AGCAGAC	TGTACTGAGGA GCCGGTG	AGGCAACACTGCTTATTAGGCCGGGCAGCCAGGAGAGAC[A/G]CACCGGCTCCTCAGTACACATT CCCCCACCCCTGCCTCGGTGCTCCCCACTCAGGGCCATGGGCAGCGGTAGGTCTGGAA	
WI-12210	76	A	G	ACTGGGAAAA CAACTATTGC A	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAACAA CTATTGCAT[A/G]GGAAAACATATGCAAACTAGCATCATTGTCTCTAGA
WI-14186b	88	A	G	...			AATGGTCTGGTTTTATTGAGAAGTCGTGTTGGTCATTGGTGATGGAAAGACAACATACGGTACAAAATTACA GGTGGTTTAGTTCATTACAATG[A/G]TACAAATCATTTACAAGTCATTAGAGTCTTTTGGAT TTT

ID	Pos			Seq 1	Seq 2	Sequence
WI-14186a	52	C	T	GGTCATTTGAT GGAAAGACAC A	AACTAAACCA CCTGTAATTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTCATTACATGATCAAATCATTAGAGAGTCTTACAAGTCATTAGAGAGTCTTGGAT TTT
WI-12234	66	A	G	GAGAACACTT GTCGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTGGTTCTAAAACTTGAGCTTGCAAGAGAACACTTGTGGGGCTT[A/ G]TTCAAACATGACTGATAGGTCCCACCCCCAGATTTCTAACTGGGTAGGTCTGGGGTG
WI-12345	37	C	A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAAAGAGGAA[C/A]CCTGAACCCCTGCAAGTATTCTCT TTCCTGACCCAGCTGGGCTTGCGCACTTTGTGAGATTTGCAAAA
WI-13416	71	C	A	AAATTTTTGG AAGTTTTCAG AAA	AGTGTTTATAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTATTTCAAATTTTGGAAGTTTTCAGAAAAAAATAAAATGACAAGAAACA CATA[C/A]AAATATTGAAATTATTCATTGAACTATAAACACTTAGCAGAGGAAGGGACTTTTGAT
WI-12310	46	G	A	TTATTCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGGTCCT AAA	TTTGAAAAGATGCTGAATTTATTCCCAAGTATAATTTAAAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTACACATACAGAATTTCAGTTTACAAATATTCCAGAAGGCATTTCTTAAGCAG T
WI-12086	72	C	T	CCGGGAAAAC TTGGATTT	GGAGTCTTCGG GTCTTGG	GAACCGAGCTTTATTGGAGCAAGAGAGTGTGGACACTGTTTACAACAAAACGTTTCCGGGAAAACTTG GATTT[C/T]CCAAGACCCGAAGACTCCTCCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T	G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGTATTTGTTAAGAGTTTGTCTATCTAAATTTCATATTTATTGGCATAAAGT TCTATAATATTCTTTATGATCTTTAAATATCTG[T/G]GGGGATTTGTACAGACTTTCCTC
WI-11585	79	T	C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTCC	TTAGAAGGAAAGAAGAAATAAAAACACGGTAAGTGGAAAATCAGTTCAGAGGTAGGAAGAAGCTGGGTT TGCAAAACAAAA[T/C]GGAAGTATCAGTGAAGCATGGCCTAGAAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G	C	...	...	TTAGTTGGTTCCTGAAACTTTATGCTGTTTATTTTAACCAATAGGATGTTCCAGTTACCAGCATTT[G/C]AGAACTAGGGACTTTTCCATGAAAAATAATTAAGAGCTAAGGAATTCTGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C	A	...	...	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAGTAAAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCCACCCTGGACTTGCCAACTTTCACTGTGAAACTGCAA[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A	G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAGTAAAATCCAGAAGACTCAGCTGCTTG[A/G]GG CATGTTCCCACCCTGCCAACTTGCCAAACATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T	C	...	...	TTGATTTTACTAAGGTCTTCCACTGGAACATGAGAGGTAGGGATAAGTGTACAGGATATAATATACTCAG ATATTTTAAAATAAA[T/C]TACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAAATTGGCAATGA

ID	#					
WI-11626a	39	G	A	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCTTCCACTGGAACACATGAAGGTAG[G/A]GATAAGTAAGTGTACAGGATAATATACT CAGATATTTTAAAATAAATTACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAAATTGGCAATGA
WI-11627	23	T	C	CCTTTCCTTCC ATTGTCCTC	CATTTGCAACC CATCTCAAG	ACCCCTTCCTTCCATTGTCCTCT[T/C]CTTGAGATGGGTTGCAAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCTTTTGTCTGGCTTACTTCCATTCGCATGTCAAGTCCATCATG
WI-11636	61	A	G	GGACTTAAAA AGATCTGCTTA TCCT	AGAAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAATACTATTGTAAGGTGGACTTAAAAGATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTGGTA
WI-11537	119	C	G	ATTGCTCATCT TACTCTGACCA T	GACCCAGCAA AAAGAAATGAT T	GTACCATTTCTTATGGTGGCAAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTACAG TATACAATATTAGAGAATATTATGTTGCAATTGTCATCTTACTCTGACCAT[C/G]ATAATCATTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G	C	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAGACTATTCAGCAACTG[G/C]AAACTGTCCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATACTCTACTCAGAGTTCACACTCATATTTTTT ATTTTGGGTGTGGGT
WI-11656	28	G	A	ATTGATTTTAG AAGGAACTGC AA	CAAGGCTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGCAGTTGTTT AAAATGTCCTGAAACAATCAGATTCCCAGCCTGGAT
WI-11680	55	T	C	…	…	ACAGATACTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCTTTT[T/C]TTGCATAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTTT
WI-11696	47	T	C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACTTTATCACAGGGGACAGT[T/C]AAGGTTGGCTTCTCTA ATGCCCACCACCATCTGTGTTTCAGAATCTTCCACTTCGCC
WI-11702	69	C	T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTCAATAATTAAAAATCGAATAATACTGAAATAACCACAGC AGTC[C/T]TTTCAGTATAATTTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTTGTTTCTGCAGA
WI-11706	60	C	T	TGGCTGGAATT TTCTCTTCTT	ATCACCAAAG AACAAATTCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTTCTTGTACAATTTATTTGC[C/T]GGCTG GAATTTGTTCTTTGGTGATTTGTCCCCTTGTCCCCTTGCTGCT
WI-11709	105	T	A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTTACGGG	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAATTAGAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C	A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTCCCAGCACAACAGCCAGCCCACACTCTAGACACGCCTTCAC TCCAGTCCATTCTGCGCACCTAGCCTCAGTCTTCAC[C/A]CTCCTCCCTCCTCCCACACTCCTTC

ID	Pos					Sequence
WI-11715b	123	C	T	AGGCTGGCTGC AGCTT	TCCCCATCCTG TGGCT	AGAATGGGAGCTGTTGGGGAGGAGGGGACATGCACACAATGTAAAACAGACAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCGAGCTT[C/T]AGCCAC AGGATGGGGACTGGGGAAGA
WI-11715a	49	A	C	GCACACAATG TAAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGGAGCTGTTGGGGAGGAGGGGACATGCACACAATGTAAAACAGACAAA[A/C]TGCATTACAACTG TGGTGTAATGTGGCCACTATGAATCCCTATGAATCCCTATGTATAGAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGGACTGGGGAAGA
WI-11727	43	G	C	AACAATCCTT AAAAACAACTA TCAACA	CCTGTGGTTTG TGTTGCAG	CTGGAATTCCTATACCTAACAATCCTTAAAAACAACTATCAACA[G/C]CTGCAACACAAACCACAGGC AAAATGAAAAACAGATGCCCCAGACAGCACCCACCACATGGCACACAC
WI-11728	16	C	G	...	...	TTTTATTATCAAACT[C/G]CAATTCCATTTCACAAATGTAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTCTTATCTCTTCCCACCCTACACTTTCTCTCCCTACAACCCGGGTTCCAAA
WI-11758	61	A	G	ATCTGTGTGTT TCGCCTG	TGATTGGCCCT GTGGTCTA	TTTTTCCTCTTTTATTAAGTCCGCTATACTAACTAGAAGGAGAATCTGTGGTTTTCGGCCTG[A/G]TAG ACCACAGGGCCAATCACCACAGCTTCTGTGAGAACATGGAGAGTGCCAAGATCACCATCA
WI-11295	37	A	G	GCCTCACAAA GTATTTTCTAA AATATAA	AAAAGTGCTCA TCTGTGTGAACTC T	CCGGCCTCACAAAGTATTTTCTAAAATATAATTTGCT[A/G]TAGAGTTCACAGATGAGCACTTTTCA CATTAGGTGATATGCAAACAAATCACTATTGGCTCAGCAGGAAACAGACTTT
WI-11773	93	T	C	...	...	AGCACATGATATTCTGCCTGGAGTTTCTGTGAGCTCAGCAAACAGAGTCAGAGATTAAGAATT ATTTATTGCCTCCTTTTTCCCCT[T/C]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C	G	GGCTCAGAGA AAACCTCTG	AAAACTCAGA CTGTAAATTT GTGTG AGA	CATGACAACCTCTTTATTAATGGCTCAGAGAGCAAGGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTGCGCGCAGAGAGACCCCTCCACCTTTTCATGCCTGTGTGTACACACTGTCCAAGCCTC
WI-11790	28	A	G	CCCAACTTACC AAACCTCTG GCAAGGGAA GCTAAGC	CGGTAGGCGAG	TAATTCACCCAACTTACCAAACCTCTGT[A/G]GCTTAGCCTGCGCTCGGCCTCCGCCTACACGTACACATGCTCAGAGCAC TTACATTAACCTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C	A	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TTTTAATTCCCAAAGCTTACAACCATCTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GTGAGGTATTTAGTATACAG[C/A]AGTCAACTATCCAGACAGTCCCATCTA GATTTTCTCTTTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C	T	GTTTTAATGT GGTATTAGAA AAGTTTAAA	CAATTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTCCATTTCCTCCCCTTTATAGTTTTAATGTGGTATTAGAAAAGTTTCTATAGACAATCTGA ATGTGGCTTATATTCTA[C/T]TTGACAGCACAGTTCTTCAAGTTGCTATAGACAATCTGA AAATTGGGTTCTGAACT
WI-11906	52	A	G	TGTTATAACAT CAAAGAAAGA ATCTGAA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTTGTTATAACATCAAAGAAAGAATCTGAAT[A/G]TGAGGGAACTG CAGAAATTAAACTTTCAGTCTGTCTAATTCTCAGAATGCCAGAGTAAGATGAACCCTTTACAG

ID	Position	Allele 1	Allele 2	Sequence
WI-11909	78	A	G	TTTGTGTTGGG TGGTCAAG — CCTCCTCTGAG ATTTCTGAAT AG — GCAGTTCTCTGAAAGAGACAATGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTTGGGTGGTCAAG[A/G]CTATTCAGAGAAATCTCAGAGGAGGACAAATGATAGTGCACTGCGAGCCAGCTCGGACTGGCTTGCAAGAGTC
WI-11806	60	T	G	CATGAAGAGT GGGCAGTTCA G — TCCTGTAAAGC CAATTTTATAT ACTAATAA — AAAAATACCATTTAGCATCAATTGCCCCAAGTTTGGCAGGCAGCATGAAGAGTGGGCAGTTCA[T/G]GTTTTATTAGTATATAAAAATTGGCTTTACAGGAAGCATTATGG
WI-11946	31	C	A	... — CCCTAGTGAATACAACCTTTGTCCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACTTCCTAGGCTGAGCTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGGAA
WI-11965	65	T	G	TGAAGATCAG ATCTCTGGTTT ATTT — CAGCTGTGGTG AATGTTGAT — ACAAAAATTCACAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA[T/G]ATCAACATTCACCACAGCTGAAGGAAATTAAACTGAACCT
WI-11027	90	T	A	TGCCCTACTAC GCTTTAAAAA A — TGAGGAAATGT GTTACAGTATT TTTATT — ACCTATTTTGAAACTGCAGAAAGGGCAGGACAAACAATCACTTCATAGATTTTTCTGGGAAATATTGCCCTACTACGCTTTAAAAA[T/A]AATAAAAATACTGTAACACATTTCCTCATTTCTTACGAATACTTTCTTTGATATTGCAAATTCTATGGCATACACAGAGCCACCTCCTCAATGCCCTG
WI-11049	95	C	T	... — TTCTGCTGAAGATCACAAAACAATTCAACCTCTGTGGTTCAAAATAATTAAGGATCTTGTACCTTTGTGTTTATTTCTGTTCAACTAAGGA[C/T]GAGACTTCAGAAGGCATAGCTTCCCTGTAACGTTTTAAACATCTTTTCATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69	C	T	AAAAGGACAG CCAGATATCA AC — TTTCCATCTTA TTTCATTTCTG TAAC — CAACAATTATCAAACATGGTAGGGAAAAGTTCTCACTCTGCACTATAAAAAGGACAGCCAGATATCAAC[C/T]GTTACAGAAATGAAATAAAGATGAAAATTTTAACAAATTG
WI-13654	49	A	G	AACAGTTAAT GAAACACATC CGT — GGCTGGTGAAA TGATGTCAT — TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGTA[A/G]GTATGACATCATTTCACCAGCCAGCTACTTCCATGTGGCAGAAAGGTAACCTTTTCCCCATTTACAGACAAAACCAGT
WI-11070b	135	C	T	... — ATGAGACCCTGCTTTGAACGTTTGGAATAATGAAAATCAGCCAGCTATCTCTGGGTGCAGAGAGGTACTCCAAGTATCAAGTAAAATTGTGACTGAGCAGAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTAC[C/T]GTGGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAGGGAA
WI-11070a	110	G	T	CAGAAAATCA GCCAGCTATCT T — TTGGAGTACCT CTCTGCACC — ATGAGACCCTGCTTTGAACGTTTGGAATAATGAAAAAGGAGCTAGGACAATTCTTGCTTTCAAGTAAAATTGTGACTGAGCAGAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAAGTACCGTGGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAGGGAA
WI-12020	121	T	C	... — AATCTTTATATTTCCAGCTGTTGAGACAGTATTTTGAGGCGTGATGTTACCTCTAGGCGGCGAAACCAGAGCCAGCTAGTAAAGCTATTAAGCAGCTACAGTTAATTGAATACATGACCATT[T/C]CTCTTTTAGCACGTTCTTTGTTCCTC

Marker	Pos	A1	A2	Primer 1	Primer 2	Sequence
WI-11076b	142	G	A	...	...	CATGGTTCTGCCAGCTTACAGGAGAGCATGGTGCTGCTGGCATCGGCTTATCTTCTTGGGAGGCCTCAGGAAACTCTGAATTATGGCAGTAGGCAGCAAAGGGGGGAGCAGGCATGTCACATACCCAGAGCAGGAGGAGAGAGAAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTCACTGTCATG
WI-11076a	106	T	C	AAGGGGGGAGCAGGCA	TCCTGCTCTGGGTATGTGAC	CATGGTTCTGCCAGCTTACAGGAGAGCATGGTGCTGCTGGCATCGGCTTATCTTCTTGGGAGGCCTCAGGAAACTCTGAATTATGGCAGTAGGCAGCAAAGGGGGGAGCAGGCA[T/C]GTCACATACCCAGAGCAGGAGGAGAGAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTCACTGTCATG
WI-14263	49	T	C	CGCAGAAAAAGGCATATTCA	GGTTATTCAAAAATTAGTATGGGACA	ACCTTTAAAGTTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[T/C]GTCCCATACTAATTTTTGAATAACCTAACTCTCCCTTGTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-14267	28	T	C	...	...	AATTATTGCTGAAATTAGGAGGGGAGCA[T/C]TGAAATGGGAAGGGGGGAGGTTAGAGAAGACAGAGATTTAAAAGAAGCAAGTACCATTTCCAAGTATAAAACTCGTA
WI-13892	50	G	A	CTTTTCATTTTTGCTTTTAAATAGAAC	TGATGATGTCATATACTAAAAATCAAAG	GATTTGTTTATTCATTCTCGCTCTTTCATTTTGCTTTTAAATAGAACA[G/A]CTTTGATTTTTAGTATATGACATCATCATGAATTTTCTCTTACTTGTATTTAGGCTCCACCTCAGTAGTTTGACAAAGGTAGAATGAGTTCA
WI-15288	108	C	G	CATGAGAGGATTCCCTCTCTC	AAAAGCTTCTTTCCCTTGGA	ACCTCTTCTGATGACACTTGTACCTGTAAGGGGTCTAGAGAGAAAAGAGTAGTAGACTCCTACTTTGCTACAATTCAGGATGCAGGGCATGAGAGGATTCCCTCTCTC[C/G]TCCAAGGGAAAGAAGCTTTGGC
WI-13951b	88	G	C	...	...	AATAAATGGAAGAGGAGGAGTGAACAAAGTAATGAACAAAA[C/T]AGACCCCAGATCAGAGGAAGAGATGGCTTTCTTGTTAATTCTGGAGCAGCAAATATTACTGAACACTTGTCTATGTGCTGG
WI-13951a	39	C	T	GGAGTGAACAAGTAATGAACAAAA	TTCCTCTGATCTGGGGTCT	
WI-13264	25	G	A	AAAAAGGGCTCTTGCCCAT	GGAGGGGAGAGACGGGAATAACTGTCTTGTCAATGGC	GAGACCAAAAAAGGGCTCTTGCCCAT[G/A]TATTCCCGTCTCTCCCCTCGACTGACCCCAGTGTCTTACAATGAAACATCCCTCAGCCCATGGCATGGTGCATCCCTTCTTGGGATCTGTGAATATAACCAACTGTCTTGTCAATGGC
WI-13960	39	A	C	AGCAAAAGGAAGTTAAATACTGATAGA	CATGAAAGGACAAATTTGCATC	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAATTTGTCCTTTCATGCATTTGTGGAGCAAGTACTACTAACTTGTTCACTGTCATTCCCCTCACAAGGAGTTGAGCCCCTAGATGAC
WI-15843	62	C	T	ATCTTATAACCAAGAAGCCTTCAG	CTCTGGCTCAGACTTGCTCT	AACTCTTATTGTTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAAGAGCCTTCAG[C/T]AGAGCAAGTCTGAGCCAGAGGTTTATCACACTTGTCCTCAGGGTCCACCAGGAACCAGGTCTTGGCT

ID	Pos	A1	A2	Seq 1	Seq 2	Sequence
WI-13983	52	G	A	TCTCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCCAGTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGATAATGCACTCACTGACTTAACACAGAATTAGAACATCCAGGCACTCACTGAGA
WI-13850	51	A	G	AATCTCAGGG TCACAGCTTTA TT	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTTAACACAGCCAT[A/G]TTACAAACATTGT CAGGGAACACATTTACAAGAATAAATAAGATGGACTTGCAGGTGTAAAAGATTACACTTCA
WI-15295	27	G	C	TGTCAGTTTGA ATGTATTCCTG A	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTTCCTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAAAGGCCCGAAAATATGAGTGAGACTCA
WI-14284	55	C	T	---	...	ATTTCAAACAAATCCAGAAACCAGGTTCTCACACTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAAATAAAATGCTTATCCAGTGGAGCGGCTCCCCTGATGCATTGA
WI-14288	85	G	C	CCGCTGCTATT CCCAGAT	GGTCCCTTCC ACCAAATCT	ATGACCAGGAGCCCTGTTCTATATGAAGAACAAACAGGTGGCCATACTTGGGTGGGAGGGATA CCGCTGCTATTCCCAGAT[G/C]AAGATTGGTGGAAGAGAGATGACACATGCAGAAGATGACAAAACGG
WI-13522	33	C	T	TGATGTAGTTA CCCCACTAAT ACAAC	CATAATATTTG AAGTCAGTGGT TCTC	TTTATTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACTGACTTCAAATATTATGAGAG AAAATTACTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T	C	CACAAACATT TATTGAACAG TTACCA	TCTATACACTT CTCACTCTCT GCTT	AAATATGATTCCATTCCACAAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCCTCGAGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G	A	---	...	TTATTTGTCAGAATTCCAGAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTACTAC TTTGAAAAGGAAACTATT[G/A]ACAAACAAGTATATATTCAGGAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T	C	---	...	TGAAAGGATACAGAAAAAACTCAGCGAAGT[T/C]GAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTTCCCAGTTGTCCTCCCCATTACACTGGACTTACACTTAATTTCTCAGCA
WI-13373	52	G	A	---	...	TTTTATTGTTGTGAGAAAAACAGGCTCTTAACACTGAATAAACATCTCAC[G/A]AACTGTCGCTC CTAGATTACAAAAAGTCAAAACAATTCCTTGACGCGGGCCCTTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A	G	---	...	TTGGTTTTAATACCTCTTGTTGGGATAAAAGGACATTGTTTTCATTAGCTTGTCTTCAAA[A/G]GAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAAGAAATTAAGGGAACAGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A	G	TTAATACCTCT TGTTGGATAA CAATG	GAAGACAAGC TAATGAAAAA AAGG	TTGGTTTTAATACCTCTTGTTGGGATAAAAGG[A/G]CATTGTTTTTCATTAGCTTGTCTTCAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAAGAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

ID	Pos	Allele 1	Allele 2	Allele 3	Sequence
WI-14297	86	A	T	G	AATGTTGGGT ACTTTTTCCAA G / TGTGCACATTC AGAAACATTTT AAACAGTCGACT / CTGACTTTATTTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAAT GTTGGGTACTTTTTCCAAG[A/T]AAAATGTTTCTGAATGTGCACACTAGAATATGCAGAATCCTTT AAACAGTCGACT
WI-12229	89	T	G		CATGTGCACA AAAAGAGTAA G AAA / ACATGTGAATT GTCCCAAAAA / TCCATGTAAATATTCTCAACAGAGAACACTATCTTAAATGAAGGATTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCAAAAAAATTAAAGATTTTGGGACAATTCACATGTTC AAAAT
WI-13582	43	C	A		TGCAATCTAG AGACTGGGGA G / TCTGCGCAGTT AGATTCCA / AAGGCTGCCCCTTACTGGACCAATGCAATCTAGAGACTGGGGA[C/A]TGGAATCTAACTGCGCAGAG AAATCAAAGACCGATGGTGTGAAATCTGGGCAGCTTCAAAATTTCTGCCTCCTAAAACATTTCAC CCAATTTTCATTATTGCC
WI-13857	28	A	G		... / ... / TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAATTAACCAAATGT CTGCCCCATTTTTGTGTAGCTTTCATACAGTACAGATTTCATTGATGTCGCTCCCACATCTG
WI-15809	77	T	G		TAAGGTAGCTA ATTCAATGTTT GTAAA / TGGTTTTCTGT GTGTAAATGCC GTAAA / GTTTTAAGTTGCAGAGATGTGAATGGTTACAAATCTGAAGCTGAAGTCAATCTTTGGTTTTCTGTT GTAAATGCC[T/G]TTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCATT
WI-15892	123	A	T		... / ... / TTAATCAGTCTGTGTCAAGAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACCCACTCTATCAGCA TAGCAATTTAAGGATCAGAGCTTGTTACATTTGTCTAAAACCAAGAGAAGGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81	T	G		CATACTCCACT CTAGCTGCAGT AGAAGAGTGG AA / AGAAGAGTGG ATGGGATGC / TCTTTTATTCCAAGAATGGGAAGCGCCATTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTCTA GCTGCAGTAATAC[T/G]GCATCCCATCCCACTCTCTCTTTTGACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24	G	A		TTTATTCCAAG AATGGGAAGC AA / TCATTCAAGCC AATGAAAATG / TCTTTTATTCCAAGAATGGGAAGC[G/A]CATTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAATACTGCATCCCATCCCACTCTCTCTTTTGACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59	T	C		GGCTGGACACT GCAGTGTGAT C CCCT / CCCACACCTGC CCCT / GCTCGTAATGAAGCAGAACGCTACAATCTGTTCAACATCTGGGCTGGACACTGCAGTGTGAT[T/C]GAGG GCAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48	T	A		TCAATAAAGA GCAGAAAGAA AACC / CAGTGTGTAAG AACATCTTTTT GTC / TTTTTTTGGTGAGTGTTGTCTTCAATAAAGAGCAGAAAGAAAACC[T/A]AGACAAAAAGATGTT CTTACACACTGAGCTTCACCCAAACATTGATATTTGCTTTTCCCGAGGGCAAAAAGA GAGTCTTCCCAGAAACCTC
WI-13789	62	G	A		TTGGATGGCTG AGGGAG / CAGTGCGCTTC CTCTGTTC / TCCAAGGAAAAGAAGAAAGAAAAACCAATCAGTGAAGACTGAATATGGACAGTGGATGGTGAGGTGG TGGGATGGCTGAGGGAG[G/A]GAGGTCCCT
WI-13594	66	G	A		TTTTTAACACA GATCACAAAA AGC / CCTTTGCGCCA GTACTTTTT / AATAACAAGTTAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTAACACAGATCACAAAAAGC[G/A]TGCACAAAAAGTAGTACTGGCGCAAGAGGACAAAATAATGCTAAGAATTAGGCCAAACAGTGC

Marker	Pos.	Allele 1	Allele 2	Primer / flank 1	Primer / flank 2	Sequence
WI-15625	40	C	T	...		GTTCTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCCAA[C/T]TGTCCCATACTAATTTTTGAATAACCTAACTCTCCCTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84	C	G	A	TCCCACCCCA CCCT / CCACACTGAA GACTCACCAG A	GTCTCACTTCTTGTCTAGGCTGTAAATTTCAGTTAACAAGTTCTTATGTGATTGTTGTGGCCACACTGAAGACTCACCAGAA[C/G]AGGGTGGGTGGGGAATACTTAATCAATATTGTGAATTTACCGATGAAATCCAGTTATTCCT
WI-13600	26	G	T	CATATTGAAAA TTGTTACTAGA TGATGG / TTAATGAGCC AAGCATCCAT	CTCACTTTAATGAGCCAAGCATCCAT[G/T]CCATCATCTCAGTAACAATTTCAATATGCACATTATATATACTGGAAACAAAGAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCTCTGATTCCCTCTCTACCC
WI-13602	89	G	T	GCATACCTCAT GACAATATTTA ATATTAAT / TCCATTCTGGA GACAACACA	GATAGGAAAGAAGAGATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCCCTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAATATTAAATATTGTCATGAGGTATGCACCTGCCCA
WI-13650	76	A	T	AAAGATTCAC AATATTTCACT TTTAAAAC / GTTTTT	GCATTAACATTTAAAAATTCTGAGGGATATTGATGAGAACTATGATGAAAGATTCACAATATTTCAC[A/T]TTAAAAACTACTCTTCATATCCTGATGACTTAAAGTTACCGG
WI-14319	83	C	T	CCAAATCATCT ATATTGTTGCA TG / CAATTCAAGG CACAAAGCTA A	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAGGAAATAGCAATTCAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGGTGGGGACAGTACAGAATT
WI-13528	80	A	G	CAATACATTT GCATTTTCCTA AAAA / CATGATACCAC AGTTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTAAACTGTAATCAATACATTTGCATTTTCCTAAAA[A/G]TTCAGAGAAAAACTGTGGTATCATGCAGGAAAAGCAGAAAAAATT
WI-13909c	93	A	T	...		ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTCCCAGTGAAGTTCATCTTCCTCACACTCTCTTCAAACTCGAATATCTTTTC[A/T]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G	C	TTCCTCACACT CTCTTCAAACT C / GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTCCCAGTGAAGTTCATCTTCCTCACACTCTCTTCAAACTC[G/A]AATATCTTTTCAGAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C	A	...		TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAATTAAAAGGGACAGAAAAATTAAGAATCAAACATCATTCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGGAGACCAGTAACTA
WI-14323a	78	T	C	ACAGAAAAAT TAAGAATCAA C ACATCA / GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAATTAAAAGGGACAGAAAAATTAAGAATCAAACATCATCA[T/C]TCTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGGAGACCAGTAACTA
WI-15389b	104	G	A	AGATAATGAA ACATCTGCGA AAA / GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGCTTGCTTTTGTCGTTTGGAAGACTACCATTATTCAAATTTATTATGTAATACACTCATCCAGATAATGAAACATCATCCAGATAATGAAACATCATCTGCGAAAA[G/A]AAGTGTGGAATCACCTCACCTCGTGTGC

ID	Pos	Allele			Sequence
WI-15389a	33	G / A	AATCAACTAG CTTGCTTTTG TC	TTTGAATAATG GTAGTCTTCCA AA	AAAATTGACAAATCAACTAGCTTGCTTTTTGTC[G/A]TTGGAAGACTACCATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAAGAAGTGTGGGAATCACCTCATCTGTGC
WI-15747	88	T / C	TGCTTCATTTT AAACTAATTT AGTGTTT	CATAATTCACC AAAAGTTCATA TAATTT	TGTAATCTGCTTACAGTCCTTTGCAAGAGACAGACATATGTTTTTGCATAAAGATATAAAATTGCTTCAT TTTAAACTAATTTAGTGTTT[T/C]TTAAACTTATTATGAACTTTGGTGAATTATGAACTGTACCAAAC C
WI-13752b	117	C / T	...	...	
WI-13752a	106	T / C	CCTTCTCGTTA AGTGTCTGGA	CCCTCCGTAAA AGGTGTCC	AGAAAAGCACATACATTTCCAGAATTTTGGAAAAGTTCACTCTGCGAGCAGCTGAATGGCAGAGATGGT CTCTGCGATGAGTTCCTTCTCGTTAAGTGCTGGATATAC[T/C]TGGCTTGCACCGGACACCTTTTACG GAGGGATTCCGGACAACT
WI-14339	102	T / G	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCACCAATCAAACAGTACAT TAC[T/G]CGGTTTCCAGAAATCTGGATAC
WI-13744	115	C / T	TGGTGCTGAAC AAAACTGAA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGAGGCCACCTGTTCAACAAAAACGTAATGGAACTTATGCAGCTTTAGAT TTCCTTTGCCCAGGTAGGAGCTTGTGTATGGTGCTGAACAAAACTGAA[C/T]GCTGTGCTATCTTTC CTGATTCT
WI-14061	68	C / T	...	...	CCTTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCGTACATACCTTAT [C/T]AACCATTTCATCCACCATTGTAAAAATCTGGGTCTCTGGATACTCAAAAACAGAT
WI-15719	69	A / C	ACCCTTTCATC CCATTCAGC	TGATACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAAACACTACCACACTGAATATGAATTAACTATTCAACCCTTCATCCATTCAG C[A/C]AATTTAAAACTCTTGCCAAGTATCATGAACTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T / C	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACACTACTAGATCAAACAGAAGTACCACAGTATGCTTTATTTGCA GGTATTAATTGGTTCTCTAAATCACCAAAACTT[T/C]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G / T	ATTTTATTCAC ATTAAACTTG CACA	GTTCTTTGATA TGTGGCTTAGT TTT	GGATTTTATTCACATTAAACTTGCACA[G/T]TAGCAAAAAATCAAAACATAAAACTAAGCCACA TATCAAAGAACAATATACAATAGAGATTTGAATTTCTCAATTGGAAGGTATTCCATAAATA
WI-13785d	72	G / A	...		TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGGTGAAGACACAAATGAAC AAGTGC[G/A]TAGTGACACTATAGCTGTCACAACAGTG
WI-13785c	56	A / C	...		TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGGAGATGTGAAGACA[A/C]CAAATG AACAAGTGCGTAGTGACACTATAGCTGTCACAACAGTG

Clone	Pos					Sequence
WI-13785b	40	C	G	---	---	TCAAAACTGCACACTATAAAAGTGTCTTTAAAATGCAGCAG[C/G]AGGAGAGATGTGAAGAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACACACAGTG
WI-13785a	27	T	C	AAAACTGCAC ACTATAAAAG TGCTT	TGTTGTGACAG CTATGTGTCAC T	TCAAAACTGCACACTATAAAAGTGTCTT[T/C]AAAATGCAGCAGCAGGAGAGATGTGAAGAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACAACACAGTG
WI-13793	88	C	G	GGATTTTACAT TCAGCCTAGAT ATAGG	GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAAATAAAAATAGTTTTTACCCCCATTGATACAACATAAGGGATT TACATTCAGCCTAGATA[C/G]AGTAACAAATCCTCCTGCCCATAAATCTATGACTTG
WI-13794	52	A	G	TTCCTCACCCT TTTCTTCTC	AGAAATGGGCTC TTAACCTTGTA	TAGTCTCCTACAATTCCATTCTTCCTCACCCTTTCTTCTC[A/G]TACAAGGTTAAGA GCCCATTCTTCAAACAAACAAAAAACAACACATAGAGCAAT
WI-15729	35	A	G	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACTTTGAACCATGTGTAGACTGC[A/G]GGCACTTTAGAAAGAAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAGGAAGGGTAAGTCCCGTTTGCAGCCCGGGCCTGCTCATTGTTA
WI-13424	66	G	A	TGAGGTTTTC ACCCTATTCTT C	TTTTTCTCCCC AGGGTCTA	GTCCTTTGCACAAGTCTCCCAACTGGTTGGAGTTTTCCCTTCTGAGGTTTTCACCCTATTCTTC[G/A] TAGACCCTGGGGAGAAAAACACATGTGTAAGTGGCTCAGGACTCAGAGGACCGTTCACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T	C	TCTTATAAAA GGTCAGAGGC AATT	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATT[T/C]GAGATCCCAGATTCAGCTTGTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTCTTGTCTGCTTTAATCCTGAACATTCTTGAAGCACGAA
WI-13446	22	G	C	GCCATGTCTT TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTCTTCACTCATCA[G/C]CCTTCTGATTTGATTTCCCTTTCTGCTCTGTAATTTTTTCTC TTCCCTTTTAGGGCCTAGTCTGTTAGAAATTCTGGTTTTGAGAGTAGTGAGCCCTTTACTTTTT CTGACTGCCTAATT
WI-13725	56	A	C	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGCC	TCACACAAAGGCCATTTGGAAATGTCACCTTACACGTGGTGAGCACATATGGGTGCC[A/C]GCCCGAG ACAGCAGGATAAGTTCACAAAACTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTCAGGATG
WI-15702d	107	T	C		---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTGAGG AAAGCATGTGAGAGAAAACTGTAACCCTGTAAAACAATACTAA[T/C]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T	C		---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTGAGG AAAGCATGTGAGAGAAAACTGTAACAA[T/C]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C	T	---		CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTGAGG AAAGCATGTGAGAGAAAACTGTAAC[C/T]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

ID	Pos			Left flank	Right flank	Sequence
WI-15702a	48	G	C	AACAAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAAGGCTTCAAAAAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAAAACTGTAACCCTGTAAACAATACTAGGGTTCTTTGAACAATAGTTT TGA
WI-13831b	113	T	C	...	...	TTTTTTTTATGGATGCACTGTTACATGTTTATTTATTTAGCGAAGGTGACTTGGAAAAGGAGATTCACAT ACTTCCACTGTATCCTCCGGGTAAGTTTCCTTCTCTTCTGTAGA[T/C]GTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13831a	56	G	C	...	...	TTTTTTTTTATGGATGCACTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAA[G/C]GAGATTCA CATACTTCCACTGTATCCTCCGGGTAAGTTTCCTTCTCTTCTGTAGATGTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13806	62	G	A	...	...	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACTAGGCCTCAGGT[G/A]C CCATTAAGCATGCTGTGAATGCAAAGGAAAAGCTTAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
WI-14372	86	A	G	...	...	CACATTTCAGCAAACAAATCGAGGTGCAAACAGGGTTTATTTCACATTAATATATTAACTGGATTT TTTGTCAAATAAATAGGGGA[A/G]TTCTCTTTAAATAACCATCTCCTCACTTCATGGCCAGT
WI-14373	95	A	G	...	...	AGGCTGTTTTTTGAGGCCTGAGGACCCCAACATGACAACGTAAGACTGTAACCATGGTCATGTGAGTT ATGAGCTAGGAACCCTGGACGAAAACCA[A/G]CACATATACAATCATCTCCCACCTCCCAACGCCCTTT ACTTTCACAGCCTCTGCA
WI-14078	61	C	T	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCACACATGGTGTATCAAAGAGAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGAGACATGCACACAAATCGAAACAAGGGCATGGGAAGGAGGACTTTAGATGGTCACG
WI-14083	47	C	T	AGACTTGAGA GCTTAAAAACA ACACT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAAACACACACTC[C/T]ATTTGTTATTTCACAG CTCAGTAGTTTAGAGGTCCAGTAGCCTTGGCTGAGTTGTTGCTTAAGGTCTTACAAGGCCAA
WI-14085	31	A	G	CATTTATTTTC ATGTGTAAGA AGAAAAA	CAGTCATGTTC ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAGAAGAAAAAC[A/G]TAACTAGCACGTGAACATGACTGCATGGATAC ACGGGCTCAGCACGAGGCTAAAGTCAGAAGTGAGTGAAAACAAAATAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCCTTT
WI-12169	121	G	C	AATAAAAACTT CCTATTTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTTGGCAAATTTATTTCCACTTATCAAGAACTTACAAAATATTTTGTTCATTTCTAAA TTTTCACCTTTATTGCTAAGTTATATAAAAATAAAACTTCCTATTTTCTT[G/C]TTTTTTTTTCA CCTCAGAACCCCTTA
WI-15705	50	A	G	GGAGGGGAGAT TTTAGACTGA AGAA	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTTGGGGAGAATGAAGGAGGGGAGGGGAGATTTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCTCTCTTGTACTACGGAGACCCTGCTATAGCCCCAACAGGAAATCCTCA TCTGCGGTTGCCAGACAG

Marker	No.	Allele 1	Allele 2	Seq A	Seq B	Sequence
WI-14379	102	C	T	TCTATTAACAGGGTTATGTCACACC	ATCATCTGTTTGAGGTTGACA	TTTATGCTGTGTTGTTGTTCTACTGGTCGGTCGGTCTGCGCTCACTAATATCCAATCCTAGTATGATTTTCTTT TACTTGTGTCTCTATTAACAAAGCAGAAA[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAAACAAAGCAGAGAAA[C/A]CCCACCATTAACAGAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCCCGCGAGGGCTGGCGCAGGACTGCCACTCCAAAATTCTTTGGAGCAGAG
WI-14102	22	C	A	...	...	...
WI-15937	24	A	G	CGCAGAGCTGCTGTATTTAAAAA	GCAGAGATCCAGACGCTTGT	ACCGCAGAGCTGCTGTATTTAAAA[A/G]ACAAGCGTCTGGATCTCTGCGAGGGGCTGGGACCAGCTGC AGTGGGGGCTCCGGCACTGCGTCCTCGGAGGACTCTTCCACCACCCC
WI-15944	24	A	C	AAAACTGAAACGTATTTCCTCCA	GGCCTTTAAGTTTCTACGGTGA	TGAAACTGAAACGTATTTCCTCCA[A/C]ACACCGTAGAAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGGGCGAAAAAAGGAAGTTTCAGGTGATACAAGAGTGTCCTGCCATCACACCTGAAGGAT GGTT
WI-14124	92	A	G	...	...	ATGTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TGTTATTCAAAATGTGTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14125	88	C	T	GGTTTGACCTGCATAGATTTTT	GGAATGGCATGGCCAC	GACAAAGAGGCAGTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGGTTGGTTTGACCT GCATAGATTTTTGACGACTA[C/T]GTGGCCATGCCATTCCTGTAAGTGAAATTAATGAACA
WI-14136	120	G	A	GCTTCTCACCATGTCTTCACAGAGACAATC	CTTGTTCTGTCTCTTTGGGC	GTTTATTTTCTCACAGTTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCCTTACAGCTGCGTGCTTCTCACCATG[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14138	23	C	T	CAGTATGTACATGTTGGCACCAGAAAAGCT	GTGACATAACATAGAAACA	TTGTTGTTGGCACCAGAAAAGCTC[C/T]ATGTTCTATGTTCTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-13551	74	G	A	TCCTTCAGTAGTAGTATATTCAGACAATC	GCTCATTTCTTTTAGTGCTAAGTAATATT	GGCAGGTTTATTCATAATTTTCAAAACTTGGAAGCAACCAAGATGTCCTTCAGTAGTAGTATTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-15953b	59	C	T	TTTTAAGAGTGTCCTTCACATC	TCATCTGTTCTTGTTGTTTTG	TTTTTTAAGAGTGTCCTTCACATCATTTATATTGTATTGCACACAAACTTTTTAACTC[C/T]GTCAA AAACAACAAGAAACAGATGAATAAGGAAGCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-15953a	26	T	G	TTTTAAGAGTGTCCTTCACATCGAT	TCATCTGTTCTTGTTGTTTTGA	TTTTTTAAGAGTGTCCTTCACATCATT[T/G]TATATTGTATTGCACACAAACTTTTTAACTCCGTCAA AAACAACAAGAAACAGATGAATAAGGAAGCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC

ID	No.	Allele	Allele	Sequence
WI-14631	82	G	A	--- TGAATTCAATGGACAGTTTTGCCTCTGTTTAGTGAAACCCTCACAAGCACTCTGCATAGTCCGCTTT CTGTCTTCTTTAAAC[G/A]TGCCTGGTTCCCTCTGCCCAAACTTTAGGATTGGGCCTCCTCAGGGCCTT GTCCTGA
WI-6053	24	A	G	--- ATCACCACCGTGTCTCAAGAACAAC[A/G]TCTTCATGTCCAACTCATATCCCGGGACTTTGTCAACTG CAGTACACTTCCTGCATTGAACCTGGCTTCCTGGAGGGAAGCCTCCTAGAGGCCAGGTAAGGGGGTGC AGCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAACCACGGAG
WI-15964	99	T	A	GCTCTCTGTCC CTGGAGGTA CCTCTTGC CAGAAACCTCTTCTGTGTATTAAGTCAGAGCAGTCAAAGGCAGCCAAAGGCAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGTCCTGGAGGTA[T/A]GCAAGAGGGTGGAGAAGTCTTGGCAAG
WI-12075	103	G	A	AGCAGCTGGG GGCAC CCCCTTCTTTC TCTTCCTTC CCT CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAGCAACAAAGCCAGGCAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGGGCACGGGGGAGGC[G/A]GAAGGAAGAGAAAGAAGGAGGGAGGAG CCT
WI-12179	96	G	A	GGAGGTACGG TGGAGGTCA TCGAATGACCC TGTAGATGC TAATTTAAAAACACGCCCTTCCCACATAGTGCGTGAGGCATCTGCACATTTTCCTAGAAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATTCTACAGGGTCATTCGAGGAGGAACAG
WI-14651	49	C	G	CAAGAATCAT TCTCATTTAAA ATTGT GGAGATATTGA TCTTTTCTGA CTTATTT CACAAATAGTGAAATTATCTGAGCAAGAATCATTCTCATTTAAAATTGT[C/G]AAATAAGTCAGAA AAAGATCAATATCTCCCCTGCTTCAAAAATGACACTCCCAATTTCACAGGTAACCACTGTTA
WI-14666	105	T	A	--- AATGTGGACTTTCAAACAAGGGTTTAAAACTAATCTTCTACAACACATTCCAGAGCAT TATAACAAGAATTATTTACAGGCAGCTAATGTATTAAA[T/A]AACCATGAAAAGAAAAAACTTG
WI-13473	31	C	T	--- ATCTAGATGTCAGCAAATGGGCTGACAAATGCCTGAGACTGT[C/T]TTGTCTGGTAGATGCAGTGTTGTATGTTTCTAC TCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGTGCAAATGTTTATATCACAGTC
WI-13967	103	A	C	AAAAGACTAC AGATACAAGG AAAATAAAAA TTGTGTTTCA TCTCCTAAAAG TG AATTTAATAGCAGCTCTGTCTGTTGTGATTTAAAGAACAAGATAAAATATGTCATTCAGCAGTCATTT AAAAAATAAAAAGACTACAGATACAAGGAAAATAAAAA[A/C]CACTTTTAGGAGATGAAAAACACAAA
WI-14408	60	T	A	GCAGACACAC TATTACAGGCT G TTAATTGTGTA AAACTCATTTG TTACTTT TTAATATTTCAGCAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAA GTAACAAATGAGTTTTACACAATTAAAATATTAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47	C	G	--- TTTTTGTGTTAAGAACAGCATTTGAAAATAAAACCTATCTGCCCATG[C/G]TTACAGCCTTTTAAAT TTGTAATATTTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C	T	CACCATGGCA CGTCCT CATTGAGATAA AGCACACTTAT CAC TTAGAAAACTGATAAAAGCAACACAACTTTTGGGGAAAGCACCATGGCACGTCCTTTTGTGCTA[C/T] GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G	A	--- ACATGGCAGATACAGAGCTGTC[G/A]TCTTGAAGCACACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTCATGATTGGAACAGTTTCCTGACCGTCTGGGAGGGGTTGAAGGGTGACCAGC ACATTTGCACATGCAAAA

Marker	Pos	Allele	Flank 1	Flank 2	Sequence
WI-16002	59	T/C	GATAACATAA AATGATCATG AGAATTTC	GCCATCCTC TTTGACTTT	CCAACACATTTAAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAATTTCA[T/C]GTTA AAAGTCAAAGAGAGGAGATGGCTAATGCATGCGTGGGCT
WI-15361b	101	A/G	CCCACTTGAAC TCAAGTCATC A	AAACTAAAAC CTTGTGCCTA AAA	GTGGAATTTATTAAGCCATCAAAATTCCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACTCATCA[A/G]TTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73	T/C	GCGTTTGACTT GTGCGG	TCCCCACTGC CCCC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTGGTTTATTCAAACTTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGGCAGTGTGGGACGGGGGAGGGATTGCAACCAGAGTTCATACTG CAA
WI-12535	50	A/T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACACATTTATTTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATAT[A/T]CTTCCTCCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCCGGTTCTTGTGTTTATCAGCTGAGAAGGCCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112	G/A	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCATTATGCTTGGCTTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTCAGAAAAAGGCACACGGGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTCCCAGACCTC
WI-12340	18	T/C	...	...	ACACAAATATAATTCCATT[T/C]CGAGTGATTAAAACCTATTGTTGTTTAGAACCAAACAAAACTAC AAGAAAAACATTTCAAAACCTTTTTTCAGGCTGA
WI-14808	52	T/A	ACCCACCACA CTACCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTAAGCAAACAGTTAAAAAGTACCCACCACCACTACCCTGTT[T/A]AAAAATCTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAAGAAAAACAACTGAAGGCCCCATGTA
WI-14816	29	A/T	...	...	AGTTAAAAAAAATCGAGTCAGCATTTATT[A/T]AAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71	G/T	...	...	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TTAGGTGATTGATTACAAATACGATCCATAA
WI-12542b	70	G/T	...	...	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]GTAGGTGATTGATTACAAATACGATCCATAA
WI-12542a	45	C/T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATTACAAATACGATCCATAA
WI-12173	57	C/T	GGATACAGCA GTAAAGAATA TCAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTCTAGAAACTGGGATACAGCAGTAAAGAATACAAAAAATCCTGC[C/T]CTTATA GAGCATACACTTCTAGAGGTGGGAAAGAGGCAATAAATA

ID	Pos					Sequence
WI-14836	28	T	C	...		TCTTTGGAGGGATAGAGGACAGAGTGT[T/C]GTTGATTTTCGTTGCGGTTCGGTTGGTTGTCATTGGTTTTGTTTTTGCTAATTTTGCCCCACCCTATAAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60	A	T	AA	TTTGTTTGCTACTTTTTACAAACTTT	ACATTCCTTATGATAGCAACAACTAAATATGATGGTGACACGGAAAAATACTTAAT[A/T]TAAGTTGTAAAAAGTAGCAAACAAAATTGAGTATATATAAGTGATAGAGGATGTATATGAAAAAGGCTATAAAAAGCTCCAAAA
WI-14863	61	G	A	...		ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAATATTTTTGTCTG[G/A]AGTTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACTATTATTGATTGCCACTACCTGGC
WI-14867	46	T	C	A	GACATTCCAAGGCTCTCTAACTGGGGCTGCAGACACTC	TTTTAATTAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCCATTCGCTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98	G	A	A	CCAAATTGACAGATATTCTGCGCCATTTATT	ACGGAGTGCTCTGATGTATTCTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGAAACAATTAGAAAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCAATGTCATGAAAAACACAAAA
WI-14898b	79	A	C	...		TTTTGTACCTATTCCCTGTTCAGTGCATGTACAGGAAGAGAGTTGTCTCATAAGGTGCCACTAAGGAAAACTTTCTCCATA[A/C]AAGCTGCCTGCGTGCCGCGTTGCCTGGGCTTTGCTAACCCCTGGTGCTGCATCTGCCTGTGTCTGTCTT
WI-14898a	50	A	C	CA	CATGTACAGGAAGAGTTGTCTTAGTGGCACCT	TTTTGTACCTATTCCCTGTTCAGTGCATGTCAGTGCATGTACAGGAAGAGAGTTGTCTCAT[A/C]AGGTGCCACTAAGGAAAACTTCTCCATAAAGCTGCCTGCGTGCCGCGTTGCCTGGGCTTTGCTAACCCCTGGTGCTGCATCTGCCTGTGTCTGTCTT
WI-14907	48	G	A	GGCACACATTGGACTCTGAC	TCTGCTGCAAGGGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCCTTGCGCAGCAGACATTGTGAAGCTGCTGGTCGGCACACCCATCAATCAGTGACTCCTGCAGAGGGGCCACATGCACGGATGCTCACGTGTG
WI-14911	52	G	A	CCAATACATTCAGTTCCTGGTC	CAAACCAGGAAAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCCAGTGCACCAATACATTCAGTTCCTGGTC[G/A]AAGGTCCTTTCCTGGTTTGCAGCAGAGATACCTTGCTGCTGTGTATCCTCCAATGCCAGAGAGAAAGAGAGGAAGTAATCT
WI-14913	88	C	A	...		CTGATGCTTTGACATCTGGGGCATTGCTGGGCA[C/A]CCTGCCACGTGCACCTTTCATATACAGATCAACCAATCCAAAACTAGTGATAGTAGAGGACTCA[C/A]CCTGCCACGTGCACCTTTCATATACAGATCAACCAATCCAAAACTACACCTCCAACCACCT
WI-14914	66	G	C	A	CTGGACACAGTTTTCTCTAGCCAATAAATTC	ATTTCCTTGATTGGCTGCTGTCGTGTAAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTCTCTAGCA[G/C]ACTTGTGGACCACACGAATTTATTGTCCTGCAGCGCTTTCACAGC
WI-14926	49	T	C	...		GTTTATTTCAAAATGACACATCCCAGATTGAAATGGGCACTTAGCGAA[T/C]ACTTGTGGACCACAGAGACTTGTGAGAACATGTTCAAAGACAGTTTCAAATAAAAATTTCCTTAATCAGGTCCA

ID	No.	a1	a2	seq 1	seq 2	seq 3
WI-16083	89	C	T	ATGTTTAACACAAACACATCAAGGAT	TGGAAAAGATTCCAGCCC	GCATCTTTATTACCACAGAAACTCATTTATGTCCTTAATCATTGTTTAATATAATATAAGCATGTTTAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATTCTATAGAAAGCACTAACCATCCATTAAAGCAG
WI-14930	55	C	T	GGAGGAGTCCCTCATGGAT	CACAACCAACCAATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTGGTTGGTTGTGTGGTGATTGGGGAGCACGGAGGGAGAGCAA
WI-14946	47	T	C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCCAGACATAACA[T/C]CTCTAAATCATCCTCTAGATCAGGAGGAGTCATAAGGACCATTAAGGCTACACACAGTACTTTATGGAAAGGATT
WI-15987b	80	A	G	---	---	ACATTAAAACAGCACAATTAAAGGGGTCCCAACGAGGTTGGTAGTGCCTTCCACTATGTGAGGATAAGGAATGGTC[A/G]TCTATGAACCAAGCTGCCGGTGCCATGCTCTAAACCTCTCAGC
WI-15987a	32	C	T	CACAATTAAAGGGGTCCCAA	GGAAGGCACTACCAACCTC	ACATTAAAACAGCACAATTAAAGGGGTCCCAA[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGAGGACACTAAGAAGATGGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTAAACCTCTCAGC
WI-14948	56	T	C	AGGGAAACTGCTAACTTGTCAATCAGTTGTTGG	GATGATCTTACGA	GAATAAAGTTCTTATTGCCGTTCCTTCAGGGAACAGGGAAACTGCTAACTTGTCAG[T/C]TCCAACAACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGTAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52	A	G	CAAAAAGCTATTTTCCTACACTTGA	ACAGGAATGTCAGAAAACAGTATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCCTACACTTGAC[A/G]TAATATACTGTTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC
WI-14958	83	A	G	AATAATTTATCTCTTTCTTTTCAAGGG	AATGCATTCATTTGGGTTTTT	GTGATTGATCTGTAATTATTATTGGGATTATTCAACTCTAAAATTCAACTCTAAAATTCAAGATGAAAATAATTATCTCTTTCTTTTCAAGGG[A/G]AAAAAACCCAAATGAATGCATTCATTTCAGTTTCTCCAGGCCTTGAACTGCAGCAGAAATTCAAGGA
WI-14976	35	C	T	GTTGATTGCTTCGTTCAAAG	TCAAACTAAATCTTCCATTCTAAGC	TATTTTTTAATTGGTTGATTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTGAGGAGGGGCAGGTTGGGGGTAGGCTCAGCGGTAGTGGCCACAAGAAGATGCCCATCTCACACCTGGAGACGTCCATGAGCACCTCG
WI-14981	31	G	T	TCAGTGGTGTTTATTGGATTTT	CACCTCTGACATAATACTTAGCATAAA	TAATTGATTCAGTGGTGTTTATTGGATTTT[G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAATAAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTCGTCACAGGAAGTTTTTGAGAGCTCACAA
WI-14992	80	C	T	TGCATTAAATGAAGCTGCAG	GCTATGTGCTCAGCTTTCCT	TGATTACATTTTTAAAATCATGCCTACCAGCCATCTAAGCCAAATTCAAACACCACTCTGCATTAAATGAAGCTGCAG[C/T]AGGAAAGCTACCAACTGAGCACCTGAGCACCTGA
WI-15002	72	T	A	---	---	AAATCTCTTCACACACAGATGAACTTTAATAAATTACAAATGCACCTGAAAATGCCTTCTTGATTTCC[T/A]TCAGTTTAGGCCTCAAGTTCCTCAAGGCTGACCTCAAAGGCCCAGTT
WI-15000	90	G	A	GACAGAAAAAGACTCAGACTGTCTAA	GTTTCTAGTTCTGCACAAACTTCA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGAGACAGAAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTGTGCAGAACTAGAAACTAGAAACAAAAATCCACCT

Marker	Pos	A1	A2	5′ Sequence	Full Sequence
WI-12323	68	G	A	CACAATACTT CATGTACCTAT GAAATAA	ATTTTGTTGATGTGGTTAAATCTTATCTCTTTTTATACACAATACTTCATGTGTACCTATGAAATAA[G/A]CAGGTAGGGAATATGTCCAGTGCAAACAGAGGACTCACACCTGTGCATAGAGCACC
WI-14683	91	A	T	AAGGGACGAT TTAGTATCTAA AAACA	CATAAGTTGCATTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAAGGGACGATTTAGTATCTAAAAACA[A/T]CAAAAAAAACACTGGGACACATGCCCCCTGAATTGCAAGTGTGTTTTT
WI-13470	100	C	A	CCTGCCTTTAT ATTGGAATTTC T	ATTTTGTTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTCTACCTGAAGACTCCATGCAGTCAAATTCCCTGCCTTTATATTGGAATTTCTA[C/A]AGAGACCCATGGTCTCCCCAAGTGAGGAAGCCGGGCACTCAGCCCTTC
WI-14712	38	T	A	TGAATGCTTCC AAGTACAAAT CA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA[T/A]CTCACAATACCATATACAACATACTTTCAATCACAACTCAAATATAAAAATAAACCTACAAAATCACATTGC
WI-13712	40	A	C	TTTACTTTGTT GTCATTTTAT TCTCTATTG	TGGGATACCCTTTACTTTGTTGTCATTTTATTCTCTATTG[A/C]ATTATAAGAAAAGTGTGAGACCTTATGGCCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTGTTGTTAAAATTTATGCAT
WI-16163	35	C	T	TCTGGTGATGC AATTGAAATA A	TCTAAGATTTACTCTGGTGATGCAATTGAAATAA[C/T]ATTGTAAGTAATGTAATTGGCAGCATTGCCCAAAGTTAAGAGAGGACTATTCTTTAAACAAAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88	T	A	AATGCACAAA ATCTTGTCTCT TC	TTTTTTTATTTGCATTGAGTGCTTTATTATATATTGGGAATTGCAGTGATATTAACATTGTACAAATGCACAAAATCTTGTCTCTTC[T/A]TGCTAGAAAGAGAGTAAAAATCTGACCTAGTTGAACAGTCTTAATGAACTCATTGTCCAT
WI-16167	58	T	C	CGGCACTCTAA ATTAGAGATA GATTTT	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATT[T/C]CATCTTATTCACCACGAGCACCACCACGCACAGTTCCACACCTGATAAATTGCACAAGATG
WI-14482	17	G	A	...	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTTCCCAAGAAACTCTGGAACCATAGTGCCTAATGCCCTTAAAATCGATACTAAAGGAGGAATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T	C	...	TGTAGTTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATTGTGTATTCCCAGTATCATGTACGCACTAAAAAAA[T/C]GTGTGCTTGCTGTGAGTGAACCATTGCTTAAGATAAA
WI-16156	97	A	C	TGAAGATTAA CCCAGAGTCGC TTTTGAAGAGA	ATCTGGTATTTGTGTATCCCAACAAGTATACAGAATCTCTATAAAACCACCCCTTCAATATGAAGATTAACCCAGAGTCGC[A/C]TCTCTTCAAAAATGCACACAATTAAGACG
WI-15012	59	G	T	GCAGCAAGAT TACATCAGTA ATGT	CATGGCAGCAAGATTACATCAGTAATGT[G/T]TACCTTACTATACTCTAGGCTATTGGAGTGTTCCCCACTACTATACTCTAGGCTATTGGGAGTGTTCCCCAC

Marker	Pos	A1	A2	Seq A	Seq B	Sequence
WI-15100	74	G	A	...	GTCACCATGTT ATATTTTCTT TAAGAC	TCTTATTCACAGCCAAGAAATACCCAATTATTCCAAATAAAGCAAAAATTGGAAACAGAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCCCTCAAGACAAGATGGACAAGACACGGCGGCAGCTGGTTCTGGGGT GCATTTCTAGTTGGACTTTAT
WI-14492	92	A	T	CCTTTATTTC CCAAATATAA AATTACT	...	TGGTACAGAATGTTAATTACAGCAGGGCAGTGATTCCAGTTAAATAAAATTAAAAACCTTTATTTT CCCAAATATAAAATTACTACAAATTAA[A/T]GTCTTAAAAGAAAAAATATAACATGGTGACAGCTTT
WI-12002c	89	T	C	...		TCTTTAATTTTTATGGAATCCAGGACACAACAAGAAAAACCACCCAAAAAACCCAAAACCACAGGAGACAGAAG ACGAGACACAACTCCTCCCCCAC[T/C]GCCTCCCTGCTCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
WI-12002b	68	G	A	...		TCTTTAATTTTTATGGAATCCAGGACACAACAAGAAAAACCACCCAAAAAACCCAGAGGAGACAGAAG AC[G/A]AGACACAACTCCTCCCCCACTGCCTCCCTGCTCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
WI-12002a	30	C	G	TCGGAATCCA GGACACAA	TGGTTTTTGGG TGTTTTTCTT AG	TCTTTAATTTTTATGGAATCCAGGACACAA[C/G]AAGAAAAACACCCAAAAAACCACCAGAGGAGACAG AAGACGAGACACAACTCCTCCCCCACTGCCTCCCTGCTCTAGAGTGGGGGACAAAGTGGGGGTGAGAC AG
WI-15116	96	C	T	GGGAGCCCTA GTTGCAGTAA ATGACA	CCTGAATATGC AATTATTTATT	TTTTCATTTATTTTCCAGAAAAAGAAATCACATTTCAGTAACAACTTACATATAGAATTAAACTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTTGTCATATAATAAATAATTGCATATTCAGGATTTTG TGAAATAGGTGATTGGGA
WI-12578	37	C	T	GGCCTAAAGG AATGGGAA	TCAAGCGACCA CCAACAC	GCAAAAGCAAAGCTATGGAGGCCTAAAGGAATGGGAA[C/T]GTGTGTGCATGGAGCAGAAGTCTTCCTGGTCCATGCAGGGGCGTCACATATTTAACTGCACTAAT TTGGGCAAACTGTCATTC
WI-15153	40	A	G	CCCTTATGTTG GCATTGCA	AACCTCAGATA AGTGCAGTGTC T	ATTTCACGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA[A/G]AGAACACTGCACTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTTCTTAATGTGTAGCAAGGCAAATTACCATTTCCTAA
WI-15215	84	G	C	TGGCTTAGAA TCAAATGGG	CCAACAGGGA AAAAGTCA	CCTTTGCTCTCTGAACTGGGACCAGGATGTGAAATAATTTTGAATCTGAGGTCGAGGTATGGC TTTAGAATCAAATGGG[G/C]TGACTTTTCCCGTTGGTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C	T	CTTGAGGACCT AGAAAGCAAA C	TTTGATTGGCA TAATCACTCC	AGGAAAGAGAGTGGTAAAGCAAAGGCGATCATTGGATGGAATGATTATGTGTCACGAGCACTTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAATTGCAAGGTTGGAGATATGCTAAAA
WI-15152	51	G	A	...		AATTTGCTAGTGCAAATGACCCAGAATTGGAAGGGCTATGTAACTACACA[G/A]TATGCACACCAC AGCCATGTCAGTGTCACAGATCCTCTTGTCATTCAGCTTTCTTAAAACACTCAAAGGCTGCA
WI-15123	55	C	T	TGTTAGTGACA GACAGATAAA TTAGGATG	TTGCTTAAGGG CAAACAGAC	TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGAAACAACATGCAAACAGCATAAATAGGATG[C/T]GTCTGTT GCCCCTTAAGCAATTACACAACTCACTGGGGAAGAAACGACATGCAAACAGACATGCAAACAGATAAAACACAAT

ID	Pos	A1	A2	Sequence
WI-15182	49	C	A	GCACAACCAG / GGCAAAATA / GCATGGGTTAA / TCCAGCA / GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAACCAGGGCAAACCAGGCAAAATA[C/A]TGCTGGATTAACCC ... ATGCTAATGGGTTACCTTTATTTAGTAATCATGGGTGCCTCATAAGCATGGTCCAGATCCG
WI-15198	38	T	C	GGGCCCTTGGC / ACTATG / ACTTATCCGTC / AGGCAGAGTAG / GTGGACCTCTACAAGTACCATGGGCCCTTGGCCACTATG[T/C]TACTCTGCCTGACGGATAAGTTGGC / ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T	C	CATTTATTGAG / TATTCTTGCTT / GTTGTAGTCTT / ACATGCTTACG / TCAAGTGGTAAATAGCCATTTATTGAGTATTCTTGCTT[T/C]GTCTCACGTAAGCATGTAAGACT / ACAACATTACGACCACCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACATTTGTCATTCAGAT
WI-12601		T		TGAT / TAGAC / T
WI-14510	104	A	T	TGGCAAAATA / TGCATAAACAA / AA / TTGAAAATGGT / TAAACTGGCA / ATGTTGAGAGTAAAATATGCCTACATATTTAGTAGTGTAAGTACACCCCAGATATTTTGGGGGAGAAGAG / TTGTTTGCTTTTGTGGCAAAATATGCATAAACAAAT[A/T]TGCCAGTTAACCATTTTCAAGAGT
WI-15239	57	T	C	CATTTGCAAT / AAACACCATC / GGACCTTATCT / GTGGACTCAGG / CAGTGTGATGACATTTCAATGTGCATTTGCAATAAACACCATCATT[T/C]CCTGAG / TCCACAGATAAGGTCCCGGAGAAAGGGGCTTCCCCTCCCTTTCTCGCTGGGTGACGTTCCCAGCGAGT / GAAGCCTTTTCTGGAATG
WI-12634	52	T	C	GCATCATATG / AACTGTCTAGC / AGT / GCATCATATGT / AAACATAGCT / AATAGC / ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACTGTCTAGCAGTATTA[T/C]GCTATTAGCTA / TGTTTACAATTGTCCTGAAGGGGTCTAGATGTGTACACCCCAGAAAGTGGTGATTCCTGA
WI-15249	34	T	C	GGGCTTGACAC / AAAGTTCTAA / GGAAAGCCAG / AGATTTTTAAC / AA / TTTGCTTGAAGGGCTTGACACAAGTTCTAACTT[T/C]GTTGTTAAAAATCTCTGGCTTCCTGGCTGG / TGAGGAGGCCACAGGCTGGGTATCCCACTGGTGCCCCGCATCTGTCCCTCCCACTCCCCAG / CCCACATTCTTGGCTCT
WI-12159	28	C	T	AAGACACCGT / GCAAATGC / CCCTCTCCTCA / GTGCACTTT / CTGTCCGGGGAAGACACCGTGCAAATGC[C/T]AAAGTGCACTGAGGAGGGGAGGGGTCTGTGACTC / CCAAACCCCTCGAATATTTTATGAATCTAAGAGTCCAGACGCAGTTCATCCACGGAGATCTGC
WI-12648	41	A	G	CCTAGTGGCAT / GTAAGGATGC / T / TTGCTACTAAA / AGTGGGACATCC / TCCCCAGATTGTGATGGAAATGCCTAGTGGCATTAAGGATGC[A/G]GTAGGGATGTCCCACTTTTAGTAGC / AACCGATGTTAATTCACTACTCCATGTTAGGTGCTTACTTGGATTATCTCACTTAAAAACCACA
WI-12684	64	G	T	CATGCTGTAA / ACAGCTGTGC / GGAACAACAA / AGCCTAAATGG / ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAATATTCAGTAAACAGCATGCTGTAA[G/T]CCATTTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGAGAGAAATTTAGCATAATCTT / T]CCATTTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGAGAGAAATTTAGCATAATCTT
WI-15260	75	G	A	AAAGGATGAA / GCTAATCATG / GA / TCTCTCCAGGG / AGCTTGC / TTTATAAGCTGAATGAAAGAGGTCGACACAGGCGGACACTGTCATAAGTGGAACAAAGGATGAAGCT / AATCATGGA[G/A]GCAAGCTCCCTGGAGAGAGAAGCTCCCTGGAGAGAGAAGCAAAATCAAGAGCTGGAGAAATTAA / TCCTG
WI-15325	39	T	C	CATGTGGCTGG / GAGCGC / CCTTCCACCAT / GATTGTGA / AAGGTTTAATGGACTCACAGTTCCATGTGGCTGGGGAGGGC[T/C]TCACAATCATCATGTGGAAGGCAAAA / GGCACACTCTTACATGGTGCAGTCAAGAGAGAATGAGAGC
WI-13936	123	C	T	AGTTGGCATTC / AATAGCCTAT / C	TGAAACTCCCA / CATGGAGTT / TATTTGATGTATTTCATCCATGGCGCTTCTCACTCCCTATACATTCTCCAGGGTTGAGGTAGTCTACCC / CCATAGGTTCAGAACCTATGCATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATC[C/T]AACTTCCATGT / GGGAGGTTTCATAATAA

WI-14528	62	T	G	TTTTAACTTTT TCTGGATGGTA CTTATTATAAA AATTAAAA	CTCGATTAGCA	TATGCTTTATTGAAGAGAAATAGGCTATTAATAATATATTTAACTTTTTCTGGATGGTATAAAT[T/G]TTGAATTATAAATTTAATTTTTATAATAAGTGCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C	T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCCA AGTCTTTG	TATTTCTTTCGGATGCAAATAAACAAAAAATTTAAAAGAAATGTGACTTCAAAGGAAAAGAACA[C/T]CAAAGACTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGACG
WI-14546	95	C	A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	GTATTTTCTGATGCTTGACATCTGGGGCATTGCTGCTCGTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGCCAATTTCTAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G	A	...	...	TTTATTGGCTGTCTCTGTAATACAACAATGTGGTGAAAAC[G/A]TCTTAATTCAGGACATCTTCCACCTTGTTTTGGCTTCCAGTTGTACTGCAAGACCAGTGTCAGGCACATAGGCTGATTAATCAGTGG
WI-14580	100	G	A	CATTCCCATCT GTCTTGCA	CCGACCAAGAT CCCTCC	AGAATTTTTCCTTTTTTAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAATACCTAGTTATTATACACATTCCCATCTGTCTTGCA[G/A]GGAGGGGATCTTGGTCGGCTTAACA
WI-8540	73	T	C	GGCCTGCATTT GGCTTA	GCCCTTCTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAAACACACAGCTACACACAGGCCTGCATT[T/C]GTGCCTGAAAAAGAAGAGGGCGACCTCTGATAAAGAATGTCT
WI-8039b	97	T	C	...	...	AAGTAGAACACAATAGAATGGCTCAAAAATATCAGAATGCCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTTCAGTTAAATATGTA[T/C]GTGTCCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCTAAAGAACCAAAGCTTAGGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATTTAATGCCGCAGCCGACCACCCACA
WI-8039a	87	T	C	...	...	AAGTAGAACACAATAGAATGGCTCAAAAATATCAGAATGCCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTTCAGT[T/C]AAATATGTATGTGTCCGTCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCTAAAGAACCAAAGCTTAGGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATTTAATGCCGCAGCCGACCACCCACA
WI-8044	107	C	A	...	...	CACAACATTCAGAAGTTTTTCTGCATTGTGTCTCTGATGTCTAAAAAGATTTGAGCTTTGACTAT ACGATTTCCCACACTGAACGCATTCATAAGGTTCTCCC[C/A]AGTATGGATTCTCTGATGATTAATA AGCCCCGAATTCTGGCTAAAGGCTTCCCACATTCAAGACATTGTAAGGTTTTCTCCAGTGTGTGGAC TCTCTGGTGTTGCACAAGGAATGGAACTTCGGCTGAATGCTTCCCACACT
WI-8550	32	G	A	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAAACTCAAGCCACAAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T	A	...	...	TATTAGATAAAACCCTTTGTTCCCGATTCAGGATGTTTAAATTGCTTCTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAGT[T/A]GATGGACGACAGCAGCAGAGAGAGTGGGGGTCTGAAAAAATGTAATCTTT GTGTCAAGGCACTCTGTGGCCTCACAACTGCGCCCCCGTCAGAGGGGATGCTGCCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGAGCGGGTTGTTGAAGCAGCCAGATGGTAAGG

Marker	Position	Allele	Allele	Flank 1	Flank 2	Sequence
WI-6192	91	A	G	GACTGCTAAG GATTTAATTTG GAT	TGAAGTGTTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACACATGATTGGCAGTTGGCATATTCTAGTGAAGCAAGTGTTCT GACTGCTAAGGATTTAATTTGGATA[A/G]ATTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105	T	A	CACATGGCAA TGATAATAAA AGAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCCTCACAAATACATTTCTCAAACTCAAACATCAAATATCTTGAAATATCACTGAACTT GTCACCAAAGAAGTCACATGGCAATGATAATAAAGAAA[T/A]ATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAAAACAATGGAATTTGGAAAAAATAGGAGTAAA
WI-6213	164	C	T	...	...	CATATGCTGCTTTATTTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTCTAACCACTCCTACAGAAGATGTTAGTATGTGTCATTACATGTTT ACTTTTGATATTGTCTCATTATACTATGT[C/T]TATATAATAAATGTAGAATACAGTAAGTAGGTGATCC TGCATTTCAGGTAAGCGGTAGGTGGAAATCCAGATTTCCTCTTGAGGAAAA
WI-6217	131	C	T	...	...	CGGGTTAAGAAATACCTTAAATTTAGGTAAATAAAGCTCAAGGAGGTGGGGCTGTCATCTGTGGTG TCAGTCCTTCTGGCCCCTGGCTGTCAGTGTGCCTCCAGGGCCTTGACAAGCAGCTCATTCAAG[C/T] GGCCCACCATGGCCTAGGGTCGTCGTCAACAAGTCCAGCAGCAATCCATGGCGTTCTCGTATATCTGATCC AC
WI-6238	175	G	A	...	...	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCCACTTCTGGTTTTGTTTTTATGCTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTGGTATTTACACAGTCAAGATACACAGTGTTA GAAACACAAAGTGTTGAGAAAAAACTTCTCAAAATT[G/A]GTTCCAGACTTCAGGAAAATGATT TCCACATGGTAAGGCAGAGTCTCCAGTGTTGGTCATCCGAAGCAGCTTG
WI-6272	86	C	T	GCATTTATTCA GGGAAAAACTT TAA	CTGTTTTTGGA GAAGACAAAG AA	CTTGATTTAATCAGGCTTTGGGGTCATAGGGGGGATTAGTCACTGTCACAGTCATTAATAATGCATTTA TTCAGGGAAAACTTTAAT[C/T]TTCTTGTCTTCTCCAAAAACAGCTGCTGGAACACCTCAAATTAA GGGATGTCATCTAAAACACCTTTACTGAAACTTGATTCCTTGGGCCAGAGGAGAGGTCTTTACTGTAG
WI-6303	96	G	A	CCCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	CAGAGGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACTTGATGCATTCATACAGGCAAGAA TCCCAGCAGCCCAGAGAAGCTCTGCGCCCTCCGATTCCCTGC[G/A]CTGCAAAGCCATGGCTGCAGACATCAGGGGAAGCT GGTGCAGTTGCAGTTCCTAGTCTGCCGATTTCCTGCCTGCCAGTCTTCTCCTCTCTCATTCTTCTGGCCC TCTG
WI-6315b	193	C	T	...	...	ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGGTAAAAGTGGGGTGCCATACA AACAGTCCCTTTCAGCCCAGCGTGTCATGCCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAAGAGTTGCTGATAGTAGTGT[C/T]AGTTGTCCTGGTT CTTCCCTTTACATTCTTTTGGGGGA
WI-6315	187	T	C	...	...	ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGGTAAAAGTGGGGTGCCATACA AACAGTCCCTTTCAGCCCAGCGTGTCATGCCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAAGAGTTGCTGATAG[T/C]AGTTGTCCTGGTT CTTCCCTTTACATTCTTTTGGGGGA

ID	Pos					Sequence
WI-6375	28	A	G	GGTTTATTGCA TATGGAAATC AA	AATGTGAGATC TTTATTCTAAC CTTTT	AAGGTTTATTGCATATGGAAATCAATAGA[A/G]TATCTTTACAAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAAGGCACATATGAAACATTTTATAGCAAGCAAGGGCAGTGAGACATCAACAA
WI-6409b	112	T	A	...	...	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73	A	T	...	...	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6523	165	G	T	GCTAATCCAGT AGAGACTGAA GCTG	AGATGCTTAGG GAGGTTGATA CAGC	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTGCAGCAGATTTCATTATAGTTACTTAA CAGCTAAATAATAAGGTGTATTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6554	195	C	G	...	...	TCTCCTAGCCCTATTAGGCTACACTGTGAGTCACTTCTCATGAGAGCCAAGGGAAACAGGAAGGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTTCTCTCTTTCACACAACTTTCCCTGAGA ACTGTCCCAGTCAGGTGGACCTTCACACAACACGAACAGCTAAAACTCTGAGAGAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAAGCTGAGAAAAA
WI-6558b	68	C	T	...	...	ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATTGTGTAATGTTCCACTTGTTTAAA [C/T]AATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTAACAAGTTGAAAAATGGGCG
WI-6558a	42	G	C	...	...	ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATT[G/C]TGTAATGTTCCACTTGTTTT AAACAATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTAACAAGTTTGAAAAATGGGCG
WI-6629	75	T	C	TCTTTTCAGAG AATAAAAGTT GTCATA	TGACACAGCAT CCATTGCT	AACCAAACAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAATAAA AGTTGTCATA[T/C]AGCAATGAGATGATGCTGTGTCAGAAGCTATCTGTTATATAAAACAGGAGCTCACAGCAGGATGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6644	134	T	C	...	...	CTGCCCCTGAACCCAATCAGATTTAGTTAAATCAAATCAATCAAAACTCCAGTCGTTTCTCTGTCTTT TTACTTAGCAAAGGAAAAACTTTAGTGAATGCTACTTGACAAGAGAAAAGTCATTTCTCAAGCACA[T/C]ACCCAAACTTGAAGGTGATTGAACCCAAATAATGGGTGGGAAACCACCAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAGCTATCTGGTTATATTTGATGTTGCCAAT
WI-6690b	106	C	T	CAGACTCTGG AGCCACAGC	ACATAAAAATA TTGCAGTGTAT TAGCC	TGCTAAACACCACCATTATTAAGGAGTACTAGGAAAAAAACTACCAAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACCAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAGAGAGCGGGTATCTGG

Marker	Pos	A1	A2	Probe	Sequence
WI-6690a	28	T	C	AAACACCACC ATTATTAAGG AGAG	TGCTAAACACCACCATTATTAAGGAGAGAG[T/C]ACTAGGAAAAACTACCAAACACAGCATGTGAAAC AGTTGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGACTGCTAAATACACTGCAATATTTA TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAGAGCGGGTATCTGG
WI-6770	53	A	G	CAAACCCCAA AACATCACA	GATGTTTAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACA[A/G]AATTATTCAT ACTATTATACACTCCAAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151	A	G	GCATTCTTCCA AAAACAAAGA A GTT	ATTCTGTAGGCAAAGGTTCAGCAAATCAGCTAGCACTAATCTTGACCAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAATTTAGATGAAATTTCACATTTAAAAACATGGTAACTCCAAGCATTCT TCCAAAAACAAAGAA[A/G]AACATTGGAATAGTCACTTACAAGGAC
WI-6761	32	C A	G	GATCTAACAG CTGCAGAATG AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG[C/A]CTTCTTCCTTCCCAGCTTTTGTGAACAAAAC AATTCTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTTGTTCAGGTACAAGGTCTC
WI-6844	225	T	C	---	TAAAATACTGCCAACTAGCATTACGTCCACTCTTGCATCATTAAAAACAAAGGGTATTCCTCCTTG GTATTTTCAAATGATGCATTATACAATAAACGAGTTAAAATGCACCCTGATTAATATG TAAACTGGTAATTTGTTTAAAAAGCATAATAATTTGGTTCCTTTCTTCATAAAATGGAAATTTAAA TATTTCTTCTGATAGTCTTGAGGT[T/C]ATCATTATGAGTAGTGCAAAGTGTG
WI-6824	112	A	G	---	CGGTTTTGCTACACTTTAATGTGGTTTTTTTTTAAGGGATTTTTTTCAGGTCTTGTCGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGCTGCCAA[A/G]CACCTTAGAAAAATTACAT GACACGGAGGAGAAATGCGCCCTCGTGCCTCCTTGAAGAGCTTAGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAATTCTTCATCCCCTAGAGCTATTGTG
WI-6889	139	T	C	GAAAAATGAG ATGCAGTTAA AATTC TCACTTTGTGG CTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGGAGAGCCAACATTCTGAAGGAAGTGTCAAGAAAACATTCTGATAGGTACGGACAA AAGAGGCTCCTCAATCAAGAGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC[T/C]AGAATAAAATTAAAAGCCACAAAGTGAAACTGTTGTTCTGGGCCCTATGTTGTGAGATT CTCT
WI-6911	216	T	C	---	TCCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACTCAAATATCTGATGAACTGAA AAGAGGTCTCCTTAAACAAGTATCATCTCCGAAGGAGAAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTTGCCTTCCCAAGGAATGTGTTTCTAATTGGTTCAAAGCACACTGGTTCC CACTTTTACCACTT[T/C]CATGACATTGGACAATATGACTACTCTTTTCTAC
WI-9413	112	G	C	---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGAAGCACCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACTTGGGTGGAGGGATGATACCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGGAAGGAG ACCATGACGACGATGACAAAACGGAAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74	C	T	---	AAAAGCTTTAAAAAAAAAAAGTGGTGCTATCTTTAGAAAACACTTTCAGCAAGATCAAGTAGCCCAGCT ACAGCCTC[C/T]GGTGCATCTTAACCCTCTCCTTT

Clone	Pos	A1	A2	Flank	Sequence
WI-9617	37	G	T	---	TGCTCTTTTATTTCACGTTCACAACACACGCCGTG[G/T]TGGCACAGTCTACCAAAGTGCCGCAG CGCCACGCTTGGGCCGGAAGGTCTCATTCTGTTCGTCTCTCTATGGACTGATTGAATTTGGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGGCACTCTGTGGGCAGAGAGGCTGAGCCCTGCCCACACTGGCACCA AAGAGGTTGCACGATGCAGCTTGCAGTGGGTCCAAGCCGGGTGTGCTGTG
WI-9657	121	T	G	---	AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTGCTGAAGTATAGCTACCATCCACTAT CATGAATTTTTGTTCATTACAAATGATAGAAAAGGCCAGATTCTCAAAATAAAG[T/G]ATAATTCTT TGTATTAAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATAATGCTTTTGATATAGATTTGAGG
WI-13119b	114	G	C	AAAAATTAAC CAGGTGTGGTG T / CCTCCCAAGTA GCTGGGA	CAGGGTCTTGCTCTGTCTCCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGTCCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/C]ACCACCACCTGGTTAA TTTTTTTAATTTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAACCAACTAAC
WI-13119a	51	C	G	---	CAGGGTCTTGCTCTGTCTCCCAGGCTAGAGTGAGGTGACACAATCAAGACT[C/G]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACCACCACCTGGTTA ATTTTTTTAATTTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAACCAACTAA C
WI-13112	71	C	T	TCATAAAGAC TACAGACTTA AGCTTTTT / TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTTCCATATAATAACACAAAATTTCTAAATATCCTAAAAAGAAAATATAAAATAGT TTCAGTATGTTATGTAGAGTCACATACTGTTGCCCGTCAAAAATATTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36	C	A	TGGTACGTGCT CTACTGATGCT GTTT / CAAAGTGTACA	TGTTAACATTTTTATTGGTACGTGCTCTCAGTACAA[C/A]AAACAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAGAAAAGCCCAAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCCTCCCCTGTGGATGAGATGAGTATGCACACAAGT AAA
WI-13020a	108	G	A	CTAATAGTGG AACCCTGAGA CTTT / CATTATTAAAC CCCTTTGCAGA	TGCTATTCATGACAGACACGTGAGACAAATATTCTTATTTACAGATGGAAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAACCCTGAGACTTTA[G/A]ATCTGCAAAGGGGTTTAATAAT GCAAATATCACATATTTCCATTTTAACACCATATTTAAGTTTTCCATTTTCTTAATAGAAAATGA
WI-12837	87	A	G	CCATATACAT ATATCAAGGT AAAGTCCA / GCCATAGGAA ATGCTGTTTTT AGTTGTGTCCA	TGTATAAAAAATCCAACTGTTCCACAAGTACATATGTCCTATGATTTTATGCATCACATCCATATAC ATATATCAAGGTAAAGTCCA[A/G]TACAAAAAAAACAGCATTTCCTATGGCCAGTGTTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAATGAGTATTTATGAAATGA

L42611b	50	G C	...	GTCCTCCAGGCCCTTCTCTGGCTGCGCGAGAGCCGGTCTTCTCAGGTTGCCTGCTG[C/C]TCTCCTGCGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCCTCAGTGCCCTCACTTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTCACATCATAATGTATTCACCA CTGGGAGCTTCACTTTGTTAC
L42611	34	T C	...	GTCCTCCAGGCCCTTCTCTGGCTGCGCGAGAGCCGGTCTGTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCCTCAGTGCCCTCACTTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTCACATCATAATGTATTCACCA CTGGGAGCTTCACTTTGTTAC
WI-1172b	179	C T	TGAAGAAATG GCTGATACCA A / ATGTGCATTT TCACTGCAG	TGAACGTGTGGTTAAAACTAGGCAATTGGTTAAAAATCAATTTAAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCACCTAGCACTCAGATTATGTTCTTGAAATACCATTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]TCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A	...	TGAACGTGTGGTTAAAA[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAAATCAATTTCTGCT GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G A	GCAGATTGGA AGTGTGAAAA CA / CACTTACATT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTCAG AAATGTAAGTGCTGCCCTCAACTGTTCTTTACCCACTAATTCTGCAATTTGAAAACTAGATTGAAT TCCTTTGCAAAACCCTTGCATCATGGAATACCGAGTTAATTAAAAGACATTAAACATGG CCTGGGTG
WI-1231b	141	G A	...	TCCATGGTTTGGTTGCTACTGACTTTGTTGCTACTGCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGGAGTGTTCACAATAAACAACACATAGGCTCTTTATTCCTCTTTCATTAATTTTCTT TCAC[G/A]TTATTCCCTCACCCTGAACGCGCCCTTCTTCCTGTAGTGACATTTTAAAATCCACTTAC ACATTCGGACC
WI-1231a	126	T C	GGCTCTTTATT CTCCTTCTTTC A / CGTTCAGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTACTGCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGGAGTGTTCACAATAAACAACACATAGGCTCTTTATTCCTCTTTCA[T/C]TAATTTT CTTTCACGTTATTCCCTCACCCTGAACGCGCCCTTCTTCCTGTAGTGACATTTTAAAATCCACTTACA CATTCGGACC
WI-472	114	G C	ACATACATAT CCATTATACA ACAGAAAAG / GACCTTTCTT TCCAGCCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAAAATCTTTTATATCTTTATTTTTAATTTTATT TTTTTTCAGGCATATAGACATATCCATTATACAACACAGAAAAG[G/C]GGGCTGGAAAAGAAAG GTCAAGTGAGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

Marker						Sequence
WI-478	46	C	T	GCATGTCTGTG TTACTCTATTT TGTTC	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTGTTC[C/T]AGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTAAACACAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAACCAAC ACTGCCCA
WI-533	29	T	C	ATCACAGCAG AGTACCTTTCT AACT	CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTCTAACT[T/C]ATAAGAGATTGTGTAGAGGTTGGAAGGAGGAGGACAGGA CGTTCTGTTGGTATAATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112	T	A	...	...	TCACTTATCTCTTTTTGTGGTGAGAACACTTAAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAAGAGAGTTCATTGACTCCTAAACTGAGTAC[T/A]CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74	C	T	...	...	TCACTTATCTCTTTTTGTGGTGAGAACACTTAAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAG[C/T]GAACAGAAGAGAGTTCATTGACTCCTAAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107	A	G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCTCGGCTTCTTCTCCACAGTCCACATGGGTCCAAACAATCCCACATTCCT ACATCCTCCCCACTGGGCTGCCTCCTCCACAACCTCACCA[A/G]ACTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36	G	A	ACTGCTTGCTT GTTGATTTAAT CCACATGACAG C	TTATTCTAATC C	ACTCACTGCTTGCTTGTTGATTAATCAACCTAGCC[G/A]GCTGTCATGTGGGATTAGAATAAAATA AACACAAAATGAAAACACGATTCTTTTTCAAGGCACACGTAAAGAT AATAACTTCAA
WI-991	37	A	T	...	...	TGCATTCATTATGCACCAAATAATAACTTCTGTACAT[A/T]CATTATTGTATTTCATTATCACAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCAACTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACACTGACTCCTTTTCTCCTTGAAAACAAGGC
WI-1011	70	G	C	CAGTATCTGA AGTTTTTGTCT CCCA	AGGAACACCTA CAAAATGACTT CT	CTTCCTGACCTGTTGCAGTGGATACTGTTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCC A[G/C]AGAAGTCATTTGTAGGTGTTCCTGGCGTTTTGCTACGTTTATCAGATGGCTGTTTTGCTGCATTCTAATACACTGC CGTCTTAAGGGAGGCTTGCAGAGCAGTTATCAGATGCATGTCTGAAG
WI-5381	178	A	T	...	...	TTCATGCAGAAGGTCCATGAGTTTACAGAATCTCAAGGAAGAAAAGGCCCCTAGAGATGACACCAGAA ATGAGAGGTGGCTTGCTCATGAAAATTGGACAGCAGTGTTCCAAGCAGAGGGAAACAGCATGGAGAAGA AAAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTGT[A/T]TTACTAAAACACAAATGT TTAACTTGGGGTCCACAAACAAGGATATGTTGGCAAATGGTATTTCTGTGATG
WI-5791b	76	G	A	...		CTATGTATTCCATCTAGCAAAGCAAGACTATTTGGATAAGTTCACAAAGATGAGAACAGGTCCTA GAACCTCAG[G/A]ATCGAAAGGAAGTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAAAATAAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTTGCACCCTGTTGT TAGGAA

Marker	No.				Sequence
WI-5791a	44	C	G	---	CTATGTATTCCATCTCAGCAAAAGCAAGACTATTTGGATAAGTTT[C/G]ACAAAGATGAGAACAGGTCCTAGAACCTCAGGATCGAAAGGAAGTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTAAAAAATAAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGCCACCCTGTTTGTTAGGAA
WI-5406c	120	C	T	---	CACTCTGCTGTTGTCCATGGGTGCCACAGAGCTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCCTTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC[C/T]TATGAGCCCACACTTCTCATTTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAAAGAGAGGAGGCAAGG
WI-5406b	118	C	A	CCAGGATGTC AAGGTGAGAA A / AATGAGAAGT GTGGGCTCAT A	CACTCTGCTGTTGTCCATGGGTGCCACAGAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCCTTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGAAA[C/A]CCTATGAGCCCACACTTCTCATTTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAAAGAGAGGAGGCAAGG
WI-5406a	42	A	G	---	CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAG[A/G]GCCACTTCCACAGATGCAACAGGCCTTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCTATGAGCCCACACTTCTCATTTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAAAGAGAGGAGGCAAGG
WI-5798	48	G	C	TG / TTTATTCTCCC TTGTTTTCTTT / ACTGTTAGAAA ACCAGTATTT TCAAT	CCATTCCTTCTTCCTCCCTCTCCCTTATTCTCCCTGTTTCTTTTG[G/C]ATTGAAAAATACTGGTTTTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T	A	TTT / TCTTCATGAAT TCATCTTTCAG TTT / GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[T/A]TAGATCGGATCATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C	T	G / TCCCAGAGAA AAATCCAAGA / AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCCAGAGAAAAATCCAAGAG[C/T]CTTAAACCATATTTGTGTTTAGAAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A	G	TGTCATTTATG CTGCAGTCG / TTACTTCCAGG CTCCAAGTATT	AAGCCAATTCACATTAGTTGATGAATTTGATGAATTTACAGTATCTAATGCATGGGCATCTGTTTCAACTCTCTGTTTTTCAAGAGGGTAGTAGGGTAAAGACTGGCTATTTTGTCAGTTTATGCTGCAGTCG[A/G]AATACTTGGAGGCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29	G	A	CCAATGCATTA ATTAGTTGATG / CCCATGCATTA ATTAGTTGATG GATACTGTAAA ATT	AAGCCAATTCACATTAGTTGATGAATTT[G/A]AATTTACAGTATCTAATGCATGGGCATCTGTTTCAAGAGGGTAGTAGGGTAAAGACTTGGCTATTTTCACAATTAATACTTGGAGGCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38	T	C	---	TCATGAGTCTTCTTCAAAGATGCTTGTTAAAGTCCCA[T/C]CAAAGAAAAGGATCCCATGGCCTAATGAAGATGTACCTCCACCTTAGGATATTTTCGAGACCAA

Name	Pos.	Alleles	Left flank	Sequence
WI-5826	134	T C	...	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTCTATTTCATGCTTCACATTTATTTTT TTTCACTTAGTTAAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTATACATATTCTTTAG[T/C] TTTCAAATTAAATGCCACCATAGAAATAAATTTCTAACCAAACAGCCTCACTCTTCCTT CCTTGGTGCATTTACTCTTTACAC
WI-5546	40	C T	CCCAATACTTT TTCAGGTGAA CCTGTATTTTA GCAAACATGGG A	CCTTATAAACCCAATACTTTTTCAGGTGAAAAAAGGGAAAA[C/T]ACCCATGTTGCTAAAATACAGG AGTATAACAGCATGACACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATTCTGATGTGGGAAATAT TAGAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT CCCAGG TGCACAAATTG	TGTTTGTTCTGCACCTCCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGATTGAGCGGGTATGGGT GGGGGTATCGGCACCAGCCTTTTTAGAGT[C/T]CCTGGGCAATTTGTGCACTAGTGTCAGA
WI-5836b	161	C T	...	TAAGTTGATTTAAACACTCTGTGCCTCAATTTTCTCACCTATAAAATAAAGATAATAGTATCTAAAA AAAAGAGAGAGAATTAAAAGTGGATAGACATGAATAACTCTGATGATACTGGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C/T]CCATTTGAAAATTAAGCTTTTGAATTGTTTTCCA ATG
WI-5573	58	C T	TGAACAGTTGG GTTCATAAGG AGAGTAATGTG AGGTGGGGA TC	TCGGGTATTAGGATGCGTTCACCCTCGATGATGGGCGTTCATAAGGAGGTGGGGA[C/T]GACAC ATTACTCTCCAACTGTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A	...	CAGGACCTTGGAGCCTTGCTGTGTTGTCCTTCCACCCTCACTCTTTCTGCCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCTCTCCTGTATGCACGCGTCTATCTTCTCTATGGGGCAATATCCATTGTCCCATTC[G/A] TTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
WI-5850a	92	C T	...	CAGGACCTTGGAGCCTTGCTGTGTTGTCCTTCCACCCTCACTCTTTCTGCCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCTCTCCTGTATGCA[C/T]GCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
WI-5612b	125	A T	CTATTAATGA GCATCGTGTCA TTC TTCTCTTGAGA AACCTAAAAC ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACATCACAAATATCTTATTTCTGCCTG TCACACTAAATTTGCAAAGCATTCAATTGATTGACTATTAATGAGCACTCGTGTCATTC[A/T]CAGTGTT TTAGGTTTCTCAAGAGAATTATGCTGTTCTTCCTGTAACTCAAGTA
WI-5612a	44	T A	...	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACA[T/A]CACAAATATCTTATTTCTGC CTGTCACACTAAATTTGCAAAGCATTCAATTGACTATTAATGAGCATCGTGTCATTCATTCACAGTGTT TTAGGTTTCTCAAGAGAATTATGCTGTTCTTCCTGTAACTCAAGTA
WI-5636	26	A C	GCCAATTTTTAT CCGCCAATAAA CATCGAGGACT TTGGGAA	TGAGAGCCAATTTTATCCGCCAATAAA[A/C]TTCCCAAAGTCCTCGATGGGAGGCATTTCAGAATCGGG GCAGGGGAGGCAGAAGGTGAGACGATGTGAAGAAC

Marker	Pos	A1	A2			Sequence
WI-5865c	103	C	G	---		TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAGAATCTTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCATCAAAAATTAAA[C/G]AAATATAATAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCTTCA GAGAAGACAGACAACTAAATAAATTCCAGG
WI-5865b	99	T	A	---		TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAGAATCTTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAAT[T/A]AAACAAATATAATAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCCATCTTCAAAAGGTCACAGTCCTTCA GAGAAGACAGACAACTAAATAAATTCCAGG
WI-5865	165	T	A	---		TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAGAATCTTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAAACAAATATAATAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGT[T/A]CCAGTCTCCATCTTCAAAAGGTCACAGTCCTTC AGAGAAGACAGACAACTAAATAAATTCCAGG
WI-5874	76	T	G	CATAGCATGG ATAATATTAT GACAGAAAAA	CCTAGTAAGTT TCAGTCATTG ATATGT	CTCAGACATTCATTTCATTAGTTGTTAATTTTGTGTATTTCATAGCATGGATAATATTATACAGAA AAAAAATT[T/GT]ACATATCAAATGACTGAAACTTACTAGGTAGCAATTGTTTGTCAATTTGCT
WI-5752	36	A	T	CAGCCTCTCAG TTTTTCCATC	GACAGAAAAG AGAGTAAATT ATGAAAAA	CATGGAGCCGACGTTCAGCCTCTCAGTTTTTCCATC[A/T]TTTTTTCATAATTACTCTCTTTCTGTC ACAATGTTCTGCTTCGTATTTCAACTCTCATTGCTGATTGGATGGTAGTCATAAAATATGGGGTGATTC AGAAAATAAGTAAATG
WI-5760b	61	C	G	---		TTAGCAGAAACAACAACAAAAAATGTCACACACTGCAGTAAAGAAGTGTTTCCCGATAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTCACACA GTTGTCTGTGTTTTAACCTCTCTAAATCCGATAAATAGCAGTTATTAGATAAGCGGTCCCACGAAA CATTGTTGAAACGAAGCCACGTTTCCGATTCACACAGTTAGTTGTCTGTT
WI-5760	187	G	A	---		TTAGCAGAAACAACAACAAAAAATGTCACAACTGCAGTAAAGAAGTGTTTCCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAAGCCGAGTTTCGATTCACACAGTT GTCTGTTTTAACCTCTCTAAATCCGATAAATAGCCATTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAACGAAGCCACGTTTCCGATTCACACAGTTAGTTGTCTGTT
WI-5944	52	A	G	TTCTCACCATG GGAATCTTG	GGGTGGGATCT AACTTGCA	AATATCTGGCCTTTTCTTCTTAGGAGGAGATTTCTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCCTCACTATTGAGAAGCTAAAAGTGTAAAGACTACTCATTTCTCAGTCTTCCTTGCTG
WI-5967b	148	C	T	---		GAGTTTAATGAATCCTGTTCCCCTCCTAAAAACCTCCTGTTCCCCCAACTTCACAATTCAGCAGATATT CTTTCATGGGTTATTTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTCAAGAGTGTGAG TAATGCTTGGTA[C/T]TTGCTCTGTGCCGTATCTGCTCCAATCACCCATTCATTCCTATTAT GCTGAATGAAACGGTTATATTACAG

ID	Pos	A1	A2	Flanking fragments	Sequence
WI-5967	165	C	T	...	GAGTTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCCCAACTTCACATTCAGCAGATATTCTTCATGTGGTTATTTGCCAAGTCATGAGGAGATGACATGTAATTGTGATCATTCAAGAGTGTGAGTAATGCTTGGTTGCTCTGTGCCGTAT[C/T]TGCTCCAATCACCCATTCCACTTATTTCCTATTATGCTGAATGAAACGGTTATATTACAG
WI-6093	53	G	C	...	GGGTAAGATCCAGAGCCACAGGTGAACTCGCCGGTATTGAAGTCTTTGGGCCA[G/C]GTCTGTAATGATCTGACTTCTCCCAGAACCCCCTCTTCTCTGGAAGTCCAACTGTGCACTGTGTAGGGAGCATTTGAACCAAAACCCAGGACACTGCTGACATTTGACTTTGACTTCAGCAAACCTTGATTGACGGTGACACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	T	C	CTTCTTAATTA AGCATCTACA AGGTACTT / TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAAAAATTGAATAATTATTAAGCACTTCTTAATTAAGCATCTACAAGGTACTTAT[C/C]ACTGTTCTGTGGGGTTTCAATCCTCTCACCTTTAGACTTCAGGAAATTCAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAATTGTCTTTCTC
WI-6450	45	T	G	CCAATGACTT ATTCTATATCT GTGTCACA / TTGTTTGAAAT GTGTGGTACTT CT	ATAGGACAGTTTTCTTCCAATGACTTATTCTATATCTTGTCACA[T/G]AGAAGTACCACACATTCAAACAAGAGCCAGGCTATGCCCAGGGTGGGATTATTTCACGGTCATGGTAATATGCATGTAAGACTATTTTTACTGGCCTTCTTTATGCATAAAACAAGGTATTGGTCTATTCAACAAACATGTGTCAATACAG
WI-6461	88	C	T	...	CAGTTGTCATGTCCCTCTGGTACTAGAATATAGTCTTTATAGAATATGTGGTTTAGAATAAAGCCACAAATTATTCTATAAAACAACA[C/T]AAGGAACGAGGCTCAAAAGTGGAACAAAAGCGGCCTTAGTTTCTAAGTGGAAGACTAAGACGATATAGGAAAATATAATCCGTGACCTCTTA
WI-7466c	141	G	A	TTTTCACAGTC TTTGTCCTGG AGTCGCATGCC AATTTATAATT / ATTGTTCCTTT	GAAACTATCCTTAGTGGTGCCACATTTCTATTTCTGATTCTTTGGTCACACAGGGACTTCTGGGCTATGAAATAGTCTATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTTTGT CCTGG[G/A]AATATCTCACAAAATTAATTATAAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGG
WI-7466b	80	T	C	GACTTTCTGGG TGTCTTTATG CTATGAAATA ATAACTAGTTC ACTGAA / TTGTTCCTTT	GAAACTATCCTTAGTGGTGCCACATTTCTATTTCTGATTCTTTGGTCACACAGGGACTTCTGGGCTATGAAATAGTC[T/C]ATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTTTGTCCTGGAATATCTCACAAAATTAATTATAAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGGATTGTTCCTTT
WI-9814	80	T	C	...	TGCTTTTTAAAAATAACAATGACCACCACCTGACACCATAGTCGTGTCTCCATTTGCCAGTCTTCCTCAGTAGAATAAGAACAGGGACTTTGCTGGCTGCTATCT[C/A]TTCTCCTTCCAGAAGAGCACTTGGCCCCCTCATAGGCCATTCCATAGATATTTGTTGAATGAATGTGCTCTTTTGCATATTGATTCCTTACATTTGATACATTCTCAGGAGGGACCATTTGGCCTAT
WI-9720b	104	C	A	...	CCTCTAACAAGAAAGAAAACTTGACTTCCTCAACTCAAAATACCCTTCTCAACTAATT[A/G]AGTAACCAAAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTAGTACATTCACCACC
	55	A	G	...	

WI-9720a	47	A G	---	CCTCTAACAAGAAAAACTTGACTTCCTCCAACTCAAAATACCCTTCTCT[A/G]ATAATTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123	A T	---	CACGCTCTAAGGCAGGATGTGGCTTATGAGATACTTGCATTGTCGTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTACCTCTCTGTCAGATGAAGGCTCAGGGTGCT[A/T]GAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTTGCATT TAAGAATTGCCAGTCTTTTGTCCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74	C G	---	CCACTTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTTCTAATTTTTATATGTTTACCCTTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACACGCCATCTTCTTTCCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTATATTCCCCA
WI-9943	91	T C	---	TGAGGCTATGATTGCAGATTTGTAGTGACTAATACTTATTAAGCAATTTCAATGTTGTGGGCACTGTT CGTTGTGTTTATATCCATCTTC[T/C]ATTTAATTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTTGCTCCCTATTTGTACCTTTAATATTGCATTTCACACCTTCTTCTTTGTCATTTAGGGA
WI-9891	39	T C	---	AGGGGCCTTCACAGATCCGTCAGCTCAACACTGCCTCCT[T/C]AGTGAGCCTGTGAACCACCCAAGAC GGCTGGTCATCAGTGTCATCCTCCTTTCCGGACAACTATCTTAAAGAAAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAATAAATTCCTTATTAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCATTCTACACAAAAGGGATTTGCAAA
WI-9897b	84	C T	---	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTGTTCTCAACATCCTATTTTCCTCAAAC ATTTATCTAGCCTGTA[C/T]AAGTCATCCAGTGAGCCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83	A T	---	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTGTTCTCAACATCCTATTTTCCTCAAAC ATTTATCTAGCCTGT[A/T]CAAGTCATCCAGTGAGCCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115	C A	---	AGATAACCCTGGAAAACTGGAAAACTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTCTTATGGGGTGCTTGGACTGGCAGGGGAGTTCAGACA[C/A]AGCCCAAGAAAAAGCC TGATATTAAGAGGCACTTGCATTAA
WI-9935a	42	C T	---	AGATAACCCTGGAAAACTGGAAAACTAGAAGAAATAATAACGTGTTGCA[C/T]ACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGGTGCTTGGACTGGCAGGGGAGTTCAGACAGCCCAAGAAAAAGCC TGATATTAAGAGGCACTTGCATTAA
WI-9983	146	C T	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCGCTCCCCATTCCTTTGTCTTGA TTCCCCAAACCCAAGGTTCTCACCCAATCTGATCAAATGCTGACTAGGTCATGGCTGGTCAGGGTAA AGCATTATGA[C/T]AGACACAAGACAAAGAGAGGTAAAGTTGCTGTCCTCAAGAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAAGG

ID	#					
WI-10019	139	A	T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTTGAGTATACAGCAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGGTTCTA ACATTCAAATAAGATCTTTTGCTTCTCTGCTCAGATGCTTTCAGATGTAATGCTATGTGAGCAAAT CTA[A/T]TCCCCTAAGCACAGTAATCAAGGCCTTCTACCCCA
WI-10020b	122	T	A	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAATTAGGC ATGCATAGAGAGAATAGCAGTGTTTTAATTGGCGAGAAAAGAAATCATGACTTTT[T/A]AAAAATACC AGACTAATGATTAAATAAATTAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10020a	39	T	C	TGTCATCTTGA CTCGTATTAA ATAAATT	AAATTCTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTA[T/C]GTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAGAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTTTAAAAATACC AGACTAATGATTAAATAAATTAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10064b	170	C	T	CCTTTAGATAT ATTGTGATTGT TTTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCCTCCTATGCACCAGATATTGTGGTGACACTCTGTTAATCCAGTATCC CTACTCCTTAGATATATATTGTGATTGTTTTACATG[C/T]GAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C	A	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATATAATTTGCAGAGCGATCTCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTAATCCAGTA TCCCTACTCCTTAGATATATTGTGATTGTTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T	C	TCTCCTGTCCC CAAACTCTT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGGATTCCTCCTGTCCCCAAACTCTTA[T/C]TTAATTCCATTCAATACAACAAGAATTTATAGAA TATGCACCACATGCCACAAAGACACCCTTATATTAGT
WI-1319	40	A	T	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACCC CTATGGT	AAGAAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTT[A/T]ACCATAGGGGTGTGTGGCTTATCT TTTACCTGGCATGGCTTTAGGTCCTGTGTATCTTTTTGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTAACATTAACACTGGTCAGATGTGTTTAAAACTTGTTGAACTGCTGCAGC
WI-10316	104	T	C	CTGTTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACTTAGTGAGGTGTAAATCAGAAGCATCTATATTATTCACCAGTCACCACCCTG GACTATAGTCTGTTGATTTTCTACCTCTTA[T/C]TAAACTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTGCACAATTTGGAGACATTCTGTGACCCCAACTTAAAACACTTCTCCCACA[C/T]AC
WI-2572	61	C	T	...	...	AGTGAGTTGTGCACACTTCAGTTACCAGGTGATGATTGAGCAGA AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

Marker	Pos					Sequence
WI-10368	31	C	T	TGAAGCAACCAGGTCTTGTT	CAAGATATTATATTTATTCTCTAAGAGGGG	GAGGAACTGCCTGAAGCAACCAGGTCTTGTT[C/T]CTACCCCTCTTAGAGAGAATAAATATATATCTTGAGATAGGGAGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTTTCTTACCCCACTGGAAGCAGAATATCCTTCAAAAGCTTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATTGCCTTTCAGGGT
WI-10391	32	A	G	CTGTCTCAGGTATGACTCCCA	GGGAGTTAGGAGTCAAGAAGTTGA	CCTCCGGTTCTCTGTCTCAGGTATGACTCCCA[A/G]TCAACTTCTTGACTCCTAACTCCCATCTCGGTGTCTGCTTCCCAGGGACGCCATCTGACACAGCCCTTTTGCTTGTTGTGACAAACAGAACATTGCAGAAGTGATGCTGCGTGACCTCCAGGATA
WI-105567c	146	A	C	GTTACCCAGAGTCTTCTAATA	TGCCGGCTTCCAGTAGCT	AGGCGATGAAATTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATATTCTTTTTCATATTCCAATTATTAATACTAGAATTTCACCAACAGAATTTTAAACATTTTAAGTTACCCAGAGTCTTCTAATA[A/C]AGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-105567b	82	A	C	...		AGGCGATGAAATTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATATTCTTTTTCATATTTCCAATTATTAAT[A/C]CTAGAATTTCACCAACAGAATTTTAAACATTTTAAGTTACCCAGAGTCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-105567a	60	T	C	GGGTGCTCAATAAATATTATTATTCTTTT	AAAATTCTGTTGGTGAAAATTCTAG	AGGCGATGAAATTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATATTCTTTT[T/C]TCATATTTCCAATTATTAATACTAGAATTTCACCAACAGAATTTTAAACATTTTAAGTTACCCAGAGTCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-11153b	84	C	G	CAAACTTCAAATTGCTTAAAGTCAGGTCTTC	AAATCCAACAGTCAAGGTCTTC	CGTTGGGAATATTTCTATCTCACCTAAATTATGCGTGATTAAAAATATACATTTAACAAACTTCAAATTGCTTAAAGTCAGGTCTTA[C/G]GAAGACCTTGACTGTTGGATTTTGAGTTTTTCTTATTCTTAATAAAACATGCATATTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTTTATGTATT
WI-11153a	33	C	A	GGGAATATTTCTATCTCACCTAAATTATG	GCAATTTGAAGTTTGTTAAAATGTAT	CGTTGGGAATATTTCTATCTCACCTAAATTATG[C/A]GTGATTAAAAATATACATTTAACAAACTCAAATTGCTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGAGTTTTTCTTATTCTTAATAAAACATGCATATTAAGTTGTTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTTTATGTATT
WI-2616	125	T	C	CACAAATGTAACAAGAATTGATCC	CCATGGCTGTAGTCCCAGT	GTTGTGAAACTCCAGTATCATTCCCTCAAACCACGCTTAAATCACAAATCACTTTTCTTCCTGTAGAGCTCAAACTCAGTCGTCAGAATGAAATGCTGCACAAATGTAACAAGAATTGATCCTA[T/C]ACTACAGCCATGGCTGTAGTCCCAGTGAAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58	C	T	CAAGTGAATTATGACCAAAATGAGA	TGTCTCTTTCATTTGAGGTTTT	TGACTCAAAGGAAACCACACACCAAAAGTTTCACCAGTGAATTATGACCAAAATGAGA[C/T]AAATTTGTTAAAAAAAACCTCAAATGAAAGAGAACAAACCTCAAATATAGTTCAAAGATTCAATATTGT
WI-10656	59	T	G	...	...	ACCTACAAAATAGGGATAGTAGTCATGGTGTTGGCAGACTTCTTTTCCTTTCTTTTTG[T/G]CTCTTAGAATCCCATTTGCTTTTGGCCAGCATTCCCTCTCCCCATATTTTAAGGAGGAATTCACCTTTTTCTGTTGGATGATCACAGGTTCTGCTCTTCTCCCAATCCAGAGGCAGGTACTATTCACCCCATGGGGGTCAT AGAGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAACC

Clone	Pos	A1	A2	Seq 1	Seq 2	Sequence
WI-11169b	154	T	G	TTAACCAAGA GTTTTCATTC TTTTT	CTAACTTAAAA ATCCTCATTCA AAATATAA	CAGCATAGAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAAATTAAGCCTAAAGTAGTGCTTTAAGCC[T/G]TTATCATGTGTTCTGATAATTTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A	G	AATAAGTGAA AGTAACTGAC TAAAAAGCAC TTGAAAAA	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAAATTAAGCCT[A/G]AAGTAGTGCTTTTCATTCTTTTTTTAAAAAAAGAGCAGACAGACATTTTATCATGTGTTCTGATAATTTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A	G	...		CAAGTGCTTGGACCTTGGATAGGTC[A/G]ACCGGCTGAAGGTTGGACAGTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTTCCTTTGGGTTACCACTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATTCCAAAATAGCCATGGGTTTGGACAAAATAC AAGGTTAGTGTCTCTCTAACTTTAATGGGCATA
WI-10686	133	C	T	CAATCTCTAAA TTCATGTGTAG ACACA	TGCCCCTGTCC AAGG	AATAACCTGTGGCACATAAGGCAAATACTGAGCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAAGCAAGATGATATAGTTCTGCTAGAATACTTGAAATCTGATGCCCCTGTCCAAGG[C/T]TGTGTCTACACATGAATTTAGAGATTGAATGAAAATGGCAAAATTCAGAAAGG
WI-11175	77	T	A	AAATGATTCTT CTGTTCTCACA TTCTTTTTTGAA AA	A	GGTAGGATGATTCTCTAGAATGCCACTTACAGCCACTGAAATATTGCCTCCCAAATGATTCTTCTG CTCAAAGAG[T/A]TTTTTTTAAGTTATCTACTATTATTATTGCTTTTTCAAAAAGAATGTGAGA ACAGTACAAAATGTGTTCAGTATAGCAAATTAAAATTAAATTAAAAGTAAGAAAAGAAGCCAATT TGGGC
WI-10694	144	A	G	TGCAAATGCTT TATGAGTTTTC AAGGAGGAAA	T	TAGAGAGGTCTTTCAGTTTCAGGGTTGGAGGGGGTGGAGTTGGAGGAGACTCACTTCTTAGAAGCACTGGC TATGTACAGAAGATAAACTCTGAGAAGAACTCAGTTCTCAAAGTGTTCAGTCTTTGCAAATGCTTTA TGAGTTTTTC[A/G]TTCCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAGCTTTCT T
WI-2716	23	T	C	TGAATTCATCC AGAAAAACAG C	TCTCTTTTCTC TCTTGTTGTCA TTC	GTGAATTCATCCAGAAAAACAGC[T/C]GAATGACAACAAGAGAGAAAGAGAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCCAGTGCATGGAGCAGTG
WI-10719	115	T	C	TGACTCTCAAG GCCATTCTAG	GCCATTCTAG AGCC	CAGGGCCCAACTCTGTCATTAAGTGTTTAGAACAGACACCTCAGTCACACAAGTTTCTCTGTATGT GCCCACCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCTAG[T/C]CGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCCATAACTAA
WI-10721	40	A	G	TGGCTCTGCTA GCTTGCCA	GAAACTCCCAC ATAAATAAAT CTCA	CAACCAATTCAGATTAATTTTTGGCTCTGCTACTTGCCA[A/G]ATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTTCCCTGCTTTAGGTTTTGAAGAAGTTGAA

ID	No.			Sequence 1	Sequence 2
WI-11204b	88	T	C	...	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTCACCTTT[T/C]ATTTAAAGTAAGTAACATAAAGGTATTATGTACATTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAATAAGTCTGAGGAAAATTATTCAGAAG GCAACATC
WI-11204a	80	T	A	GTAAAAGGG TGAAAAGAAA AACTT	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTT[T/A]CACCTTTTATTTAAAGTAACATAAAGGTATTATGTACATTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAATAAGTCTGAGGAAAATTATTCAGAAG GCAACATC
WI-10732	80	C	A	GCTGTGTCTTC ATTGGTTCACT CTTTAA	ACATGTATTTCCTTTAGTGGTCAGCCTTCCTTACCCCCAAGAATATCCCTGGTTTATTGCTGTGTCTTC ATTGGTTCACT[C/A]TTAAAGTTCTGTTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTCCA CACCACTCTGTTTAAACTGTC
WI-11206	127	A	T	GGTTGTGTTTT CTGTATGTGTACA ACTC	TAGTCTTTCTTGTCGACGAGTGTCATAAAGAATTACCACTCTGTCACATTTGTAAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTTGTTTTCGTGATGTACAACTC[A/T]CCAA CCATTAGGATTGTCACTCTCATATAGACAGAATTCAGTGGTGGATTTGAATTCCACACATGGA ATAAGTCTA
WI-11215	68	C	T	...	GAAAAAAAGTTTAATTGGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTATTTAGT [C/T]ATTTTTCTATAATATTTTCTTGTGAAGTGATGGATTTTCTATAAATTAAGGAAACAGATATT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTCTTTATTCCAAGCCCCATTCCCACCATGT TTT
WI-11219b	89	G	A	GGTCCTCTAAT TTTTCTACACT AGAGAAA TTCT	ATGAAAAATGCATTAGAAGAATTGGAGGATAAAATTCCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18	G	A	...	ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAAATTGAGAGAATATTCCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136	G	A	CATACCCACTGC CCTGGTAGCCA GGCTGG AGTTGTGA	AGCCACAGTGGAATCATTTACACTACCGAAATCAGCAAATGCTAAAATTGGGGCTTTGGATTTTTGT TTTGTTTTTCCATAGACCCCACCGTTGAACTATTGTTAAACATTTGTTAAACATTCTTGAATTGCTTTCACAGGCTACTGG G[G/A]TCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTCACAGGCTACTGG AAAGCC

ID	Pos	A1	A2	Seq 1	Seq 2	Seq 3
WI-11222a	25	C	T	GCCACAGTGG AATCATTTAC A	TTTTAGCATTT GCTGATTTCG	AGCCACAGTGGGAATCATTTACACTA[C/T]CGAAATCAGCAAATGCTAAAATTGGGGCTTTGGATTTT TGTTTTGTTTTTTCCATAGACCCACCGTTGAACTATTGTAAACATTTACCAGCATACCACTGCGG CTGGGTCACAACTTGGCTACCAGGAGAACCTGACACAGACTTGCTTTCACAGGCTACTGGA AAGCC
WI-10775	39	C	T	TTTATGCCATA TTAATTCATTA CACTC	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTTTTATGCCATATTAATTCATTACACTC[C/T]ACATCATATTTCTTAGCAAATACA TCTAGACACCTGGCACTCAGTAGGGATATCCTGGCACGATAATCATTGTTATCATTAGACATTGCA GGAACCACCATGATGGATAAATGTGTTGTTTAATGAAGGCAAGCAATTA
WI-11226	165	A	C	...	...	TTGCATGTCATTTATACGAAAGGAGAATTAAAATATCTTCCTTATAGTTGAATTTTAAGTAAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCCACAAATTAT TTCATGA
WI-10778	62	A	G	GCAAGGGAGG AACATTTACA G	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTCACCAGCAGGGCCAGGAAGGGTTGATCTGGAG
WI-10789	21	C	T	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	TGGGACACACTGCTCTAGACC[C/T]TCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGGACGCAGAGGCATCAGGGCCTTAGTCCTCCTGGGGACAGTGAAAGGGCCACCACC
WI-10810	58	C	T	CATCTTCATGG GCAGGAATT	CAAACCCTAAG AAACACAGAA ATG	ACAGAAAAAATGCCTAGGTCTTGTAGCAAGAGAGGAAAGCATCTTCATGGGCCAGGAATT[C/T]CATTT CTGTGTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCCTGTCCCCTGATCCAGCAACATT TCCGTAACTACCCTCTAGAAGTCATGCAAAGAGAAATGATGA
WI-10828	23	T	C	...	...	GGACCAAACAGAATTACTTGGCA[T/C]AGGGTTCTTAAAACTATTTCTGCAGAACATTAGTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGCTATAAATCTGATTTCTTGAGCAGGAGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91	G	C	AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCTTCCCAAGCAGCCATCCACGCTGCTCTTAGCACAAAAAAATAGAATACATCATTCTGAATG GGCACATTAATCTGCAGGCTCTCC[G/C]TTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGAGGGCAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10834	96	C	T	AGAATTAACT GTTCAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAAATGCCCAAAGACCATTAACAAGATTTAATAGTTAAAGCCAAAACTATA AAGAATTAACTGTTCAAAAGTGTGTTAAT[C/T]TGCTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T	C	...	...	GGATGATGTTCTCGCTACCCATAGTCACCTGTCCCTTTA[T/C]AAAGCCTCTTGCATCCCAAATGTGTAAATTATTTATTCT TGGTATTTCTCGCTACCCATAGTCACCTGTCCCATAGTGTTCCACCCT

ID	Pos	Allele 1	Allele 2	Sequence
WI-2296	81	A	G	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGTCTCAGGCTTTAGAAATAAGTTGTTACTTTGATTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTGCAGAGAAGTTACATTGTTTGTTG
WI-2300	77	G	T	TTTCATCATGCTGTCTTCCCTGGAAATTTCCTTTATTTGAGCGGGGCGCAGGTGGTAGGCACAGAAGCCAGTCATAC[G/T]TGCTTTAAAATTGACCCAACCATTACTAAGAATAGCATTCA
WI-2371	55	G	T	CAATGATCCCCAACATTTCCAGGGAAAGGTCTGGTCTTGTTCTTCCCAGCTTCT[G/T]GTGGTGGCTGTCAATCTTTGACATTCCTTGCGAGCTGTGTAATCCTTGCCTCCAGCTTTACATGATGTTCTCTCCGTGTGTCGTGTG
WI-2395	122	A	C	GGGGGCACAATTTAGCTACAGTGCATATTAAAAAGATAACATAGAATATCATAATAACTTGGTTACTGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTACTATCCAA[A/C]CTGAATTCAGAATAAATAGAAAGGTGAATCATCTTATATCATTAAAGAAGCTAAATTATTAGTAACAATCTTTACATTTACACAAACCCA
WI-2437c	192	G	A	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAATAATTTCAGCTTGAAGAGAGATTCCAATCACACAACTTTCTAAATAATAGACACCAAAAATTCCCAATGCTCTAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTGGTGCCAAGGACGCATTATG
WI-2437b	179	G	A	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTTCAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAATTCCCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGGCGTGTGATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGGCGTGTGGTGCCAAGGACGCATTATG
WI-2437a	128	G	A	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAATAATTTCAGCTTGAAGAGAGATTCCAATCACACAACTTTCTAAATAATAGACACCAAAAATTCCCAAT[G/A]CTCTAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGGCGTGTGGTGCCAAGGACGCATTATG
WI-2440	71	G	A	CAGTAGGAAACGGGTTCTTCCTTAGACCCCTCCAGAAAATAATGCAACCTACTGACAATTTAATTTAGTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCGAACT
WI-1356	123	T	C	CTGTAACCTACACACATCCTCCTGTAACCTCTAGGTTACTTGTAATACAAAACACAATGTAAATGCTACATAAATAATTGTCATCTATATTGTTAGGAAATAATGACAAGAAGAAAAAAAGCC[T/C]GTACATGTTTGGTACAGTTGTAACCAGCCATTTTCCCCCAATATTTCAATCCACAGTTGGTTTAATCCACAG
WI-2886	46	C	A	ACAGTTAAGAAAAAGGCTGCAGCCGTTGGGGGGAGAAGA[C/A]AACGAGATAAAGCATGGCAAAGACCACGCTGAAAGTATCCCAGGGTGCTGTATGTGCACATAGGAAGAGACTTACCTCAGCATAGGAGGAGGGCTAGGCAAGGAAAAGGTGTCAGAGAAGAAAACAGAGAGGAGCGTT

ID	Pos	A1	A2	Flank 1	Flank 2	Sequence
WI-2906b	77	T	A	...	...	CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATTCTTGCTGGAACTTTGCTGGAATGCTC TTTCCCTCT[T/A]GAGCTTTGCTTGCTTACTTTTCTTTTCCTTAGGTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGCTGACCAACAAA
WI-2906a	50	A	C	GACACCTTCAT TCTTGCTGG	AGAGCATTCCA GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATTCTTGCTGGCTTACTTTTCTTTTCCTTAGGTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGCTGACCAACAAA
WI-1736	175	C	T	...	...	TACTCCTCATTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTCCTAAAT TAGATTTCCCACCCCAGCACTATTTACACAGAAACAGCAGTTGGAGTCTGGCTCTTAGA GAACTTACTTAAGGACAGTGGTTTCCATCTGTCTTCCCA[C/T]AGAGGATCTAGGTGTCTTTGGAACC ACCTTGG
WI-1851	136	G	A	GCATTGAATT AACTATAGAT GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	AATACCCCAGTCCTAACACCATCACACACTGATCATCAATCAGGTTTAACATATTAATCTGGGGAGG ACACAAACATTTAGACCATAGCCATTGAATTAACTATAGATGTGTTAAGTAATTAATATTAACATGGTA CA[G/A]ACAACTTCAGTTTAACATTGCTAGTGATTCCATGTGGATACCATGTACCTTCTTACACATG TGA
WI-3000	62	G	A	CCCAAAACAC AGAGACCCC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTGGGAAGCACTGTCTTACATCTCTAAATGTCAGCACCCAAAACACAGAGACCCC[G/A]T GAGTCTTAGTCAATCCTATAGTGGCAGTAACCTGAATCAGTGCCTGGTCATAGTAGACACT
WI-1754	177	G	A	TTTTCTCCCTT CTTAAAGAGA TAGTC	AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAAACAGCCCTTCTCCCCGCCACCCCGGATTATTTACT TAAGGGTTTAGCAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCTCATAAAGTGATTTT TTCTCTTCTGTTGTTTCTCCCCTTCTTAAAGAGATAGTC[G/A]CCAGAGGCAATTCGACTTTCTGT AGCCACAAGATT
WI-3167	37	T	A	AAATTCAACC ACAGATCTAT ACAGATTC	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAATTCAACCACCACAGATCTATTAGATTC[T/A]ACCCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGGAGACATATTACTGGTGGAGGAAGCCAAATTCAA
WI-3208	140	G	A	GTGGAGTGGGC AGATAAAGA	TCACTCAAACT AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGTGGGCAGGTAGGGAACTTGCGCAGCAGAGAGGAGGAAG AAGTTCAGACGGTTGGGTAGGATAAGTGGATCCAACCCCTTTGTAGGGCAGGTGGTGGGGGGCAG ATAAAGA[G/A]CCAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAG
WI-1775	47	C	T	CCTGCATGGTC TTTTCTCTG	AGTTGAGATTT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAACCCTGCATGGTCTTTTCTCTG[C/T]TTACATCATTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55	G	A	AGCATATTCA TTGATTTCCTT ACAT	GAGGACTTAAA AAGGAGCATTT G	CTGCCCCTTTACATCCAAGCCAGTTACTCCGAGCATATTCATTGATTTCCTTACAT[G/A]CAAATGCTC CTTTTTAAGTCCTCAACTTTAAAGCGGAAGTTGAGACAGTGCACAAATAGATTTCCTTAGGA

ID	Pos	B1	B2	Primer 1	Primer 2	Sequence
WI-3416	33	C	T	CCAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCCAAGTTGTAGCAGCATTCAGAAGAGTC[C/T]CTCTTAGAGGTAGTTGTGCTGCGTCGTTAAAA TATGTTTCAAGATAGTAGTATCTCCCTGTTGTCACTTCCTCCAAACAAGTGTACCAACAAGCATTGTAAG GAAATGTGCAATGCTTGCTCACCTCTGACGCACAACATAATTAAATCCCATTGCCTAAAAAGACCAGG
WI-3453	70	C	T	TTCTTAGGCCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCCTACAACAACAGAAATTAACAAATTGAAAATCAGCTACTCTTCTTAGGCCCATCAGAG AATT[C/T]GAAGTCATGGGGAAAATTGATGCCATGTGAATTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109	G	A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTCCCTAATTTTAGCACACAGTATTTTAATGAGGTGGT[G/A]TGGGAGAAAATTGATGGTTGCG TAGTTGAGTTTTCTGTCCACC
WI-3474a	90	A	G	AGTCAGTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTCCCTAATTTTAGCAC[A/G]GTATTTTAATGAGGTGGTGTGGGAGAAAATTGATGGTTGCG TAGTTGAGTTTTCTGTCCACC
WI-3502	79	C	T	CCTGGGTTCT GGATGTCT	GGGTGACCCTG TCCTCA	TTTGACCCCATACATGAGAATAAAACCATAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTCT[C/T]TGAGGACAGGGTCACCCCAC
WI-3600b	146	G	C	GGTTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCGCAGCAGTGTCCTGCCTCCTGCGTGTTCCAGAGTCTGATTATCCATGCCCCTG ATAGTTCTGTGAGCACCTAAACTCGTTTCCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGGATA TAAACATCT[G/C]ATGGAAGGCTGCACTGGATGAGGTCACAAA
WI-3600a	78	T	G	CCATGCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCGCAGCAGTGTCCTGCCTCCTGCGTGTTCCAGAGTCTGATTATCCATGCCCCTG ATAGTTCTG[T/G]GGAGCCACCTAAACTCGTTTCCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGG ATATAAACATCTGATGGAAGGCTGCACTGGATGAGGTCACAAA
WI-3678	125	G	T	---		TAAATCATGCTTATTTTTCACAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATCCTTCCTGAACCTTCTACTTACTGCTGCTGTGTTATGATGCACCT[G/T]CCTTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAAGACACAATTACCTTGTGTTTCAGGCAGGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTCCAAAAGCCTTATGTCTTAC
WI-3687	67	A	C	---	---	AAAGGCGATGTTGAGATACCACATTCCATGAAAGTAAAAACACACACAAAAATATGACATAAAA T[A/C]AAAAACTACTATAGTTTATGAAAATGACTTCCAAAATTCAGAGAAAAGTCACTTAAACAGG ATTCTCAATTCATTCCAGAAATACTCCTCTGTCATTCTTAACTTTGACTGCACAG
WI-3735	72	T	C	CCTCAGTTATG TATCAAATGA AAAAC	GGCTCACCAAT CATTGTTTT	TCTAAAATGTGAAACCAAAGAATCCTGACACGACCTAACCTGCCAGTCCTCAGTTATGTATCAAATGA AAAAC[T/C]ACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCCTTATTTAATGAAAA GATCTTGGGCAATTAACTC

Clone	Pos	Allele 1	Allele 2	Flanking oligos	Sequence
WI-1819	51	C	T	---	GAAAAAGCAGGAAGCCAGGCAGGACAAACTTTGAAAAAGTCTTTCAGCAC[C/T]TTCGTGTGGATCCGAATTTTAGTGTGTGATTGGCAGGCAATGCGGGGTAACATGTTCCAGTGTTTAACTTGCACAGAATTGCCAGATTAGCGACGGATTGTTGACTTGTCCAATTAATGAAATGTGAAAAAAAAAAGGGTGGTAACTGTTAAGCCTGCTGCTGCAATGTTTAGACACAGTTTTGACACAGTTGGGAGGTGGAATACC
WI-3746	116	G	A	---	GGCCTATTCACATGACACTGGGCCAAGATCTTGCTTCCCTTCTTCAATAGATAGACTAACTAGAAAACTGCCCTGGCCCAGGAAGATGGTTGTCTTCATCATCTCTGTCTCTGC[G/A]GCCCCAGGATAAAGCAGGCA
WI-3867	49	T	C	ACAGTCATTT AGTCTTCCTGA CAA / TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA[T/C]CGGATGTACCTAGTATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGATTGTACTTGAACAAAGACACAGTCATTAAGTGGAGAAGCCAGCAGCATTCTAATCAGGTCAGTGATCTGCCAAACAACCCTTCTGCTATAGCATC
WI-3898	25	A	C	TGACCAATGTC TTTAGAAGCA G / TCGTCGGTGTC CTCTCC	CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGAGGACACCGACGAGACACAGGAGGAGTGAGGTGAAGATGAAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGCAAGGGTTGCTGGCCACT
WI-3901	114	A	G	---	GGACCATTGTCCCTCAGAAGTACATTCAAGCCCTGACGGTGTGTCCTAACACTGTGACCTCAGGCAAGTCATGTCTGCTTCCTGAACCTGGTCTTCCTCACCTGACAAGTGG[A/G]TATCATGTGCACACTGCAGTGTTTATAATGCTGCAT
WI-3914	99	C	T	TGATTCTTCTC AAGACTCACA GC / TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAAACTTTTATTACCTCCCCTGAGTTGTTGCCTTGCAAGACATTGCTGATTCTTCTCAAGACTCACAGC[C/T]ACCATCCTTCATTGCTTCTAGACCTATAACTAGACTCAAGTCCCAGCAGCCCTTAAAGGTACAAAGTGTGACCCATGGAGGTATGTTACGCTACAAAAGAG
WI-4019	33	G	A	CCAAGAGCGT CCTATGAATC ATG / AACAGCAATA ACAGGAACAA	CCACTCCCAGGCCAAGAGCGTCCTATGAATCAT[G/A]CATTTGTTCCTGTTATTGCTGTTCACAGAGTGGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGAGCGAAGGGTC
WI-4091	84	A	T	GTCATTGCATG ATT / TTGAGGTCTTA TAAGTGACAAT / TGAGTTCCTAT	TAATTCACATTGCTCTTGTTTGTGCATTTATTGCTCTCTTATGTAAACACAATCACCAACATTGAGG[A/T]TCTTAGTCATTGACATGATAAACAATATTGTCACTTAATAGGAACTCAAGCATAGTATGTGTACATTTATTGCTAACGCAG
WI-4160	117	A	G	CAACAGAA / CCTATAATTTA GCAACAATAT AGCC / TGCAGGTAGAA TTTTCTAATAT	TCCTCTTCTGTAATAGGAAGTCTGATTAGAGTGCCTTTGAGGTTAGGTTGGCTTCTAAGATGGTAATTATCTGTCCAAGTTTTGTTCCTATATAATTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAAATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATTGATACT
WI-4168	32	A	G	GGTGAGAGTC AAATTGATAC AAAACA / ATTGCCAAACA GATTTTCAGA	CGTTGCTGCTGGTGAGAGTCAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGGCAAATATATACCAGCAGTGTGGTCTAGCAATTCACTGCTGCATTAACTAACATAAATGAT

Marker	Pos	A1	A2	Sequence
WI-4177	68	T	C	ATGCCTGCGATATACTTTCCAAATGACTAGTAGTATGAATAAGCACGTATTAAATTACCTATTATATTA[T/C]CATCATGATTTGCTGCCTTCTTTCCAAATTTACTACAAATTGTATTGTCACATGAGGCACATGATCCCATTAACCCAAATAG
WI-4199	51	A	C	GCCATGAGCACAGAGGCTGAAACCACTCCCAAGTTAGTCAATATAAACAGTCCACAGCAAACAATTATACCTAATCAACATATAAATGTCAATATAGATTAAAACA[A/C]CACACATATTG
WI-5163	24	C	T	TTCTGCTGTCACTGGTCTGCCTGT[C/T]GGTCTGTGTTCCTTCAATGTTCAACTGCTTGTATCTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTTGGAAATTGCAACATTTGGGCAT
WI-4250b	117	A	G	... TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACAGGTTCAATATGAGTCTTGTGAAACAGGGGGTGGGAAGGATCCTGTAAAAGG[A/G]TAAATATTGTTTTCCATAATATTGAAGATGTG
WI-4250a	94	G	T	TCAATATGAG TCTTGTGAAAC AGG / TCCTTCCCAC / TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACAGGTTCAATATGAGTCTTGTGAAACAGG[G/T]GTGGGAAGGATCCTGTAAAAGGATAAATATTGTTTTCCATAATATTGAAGATGTG
WI-4255	68	G	C	TGCTCCCCCAT CACCT / GGCCTACTTCA AGTTGTGTAAG G / TAAATGTCTGGGGAGATAATAGGAAAGGTCCCATCCCTCTGATACCTTGGTTGCTCCCCATCACCT[G/C]CCTTACACACTTGAAGCTGAGGCCCCATCCAAAACACTGGTCAGAAGAGTAATACTGTCGAC
WI-4256	57	C	T	... ACAGCCTCTTCAAATGGCACAATCAAAAGCACCAGTAAAAGCAGAGGCAAAATCTGG[C/T]CTCACCATTGGAAAAGTCTTCTGAAGGATAAGGGACCATGTTGTCTTGTTAAATGTACAGTGACTGCTGTAGAAGAATGATTGGCCTT
WI-4325b	71	C	T	... AGTTCACTGCCTAGATGAGTAGACCATGTTGTCTTTGTAAATGTACATGGGCAGGAC[C/T]GGAAATGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTGGTCTCTTCAAGATATCCAGCCACCCAGGACACTGCCATATCT
WI-4325a	58	C	T	... TGGGCAGAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCACTTCTGCCTGTCACCTTCTCTAGACTCTTGACCCTGCAGGAGGATCCCTGCCTCCTGAGTTTTATCATCTCCCACCTCCAGCCCAGGGCCCTGTATCTGTTCAGGCCC[A/G]GAATCGTCACAACGTGTGGGAGGTAGGAGGAATGACGACG
WI-4347	158	A	G	... / G / CCAGTCTAGGCTGCAAGGACTCAATTCTGGGGCAAGTCCTGGCGCAAGTCCTGGTGTTGTTGGTAGGGTCAGAGGCAGGCGACCTGAGGGGACCACAAACCAGTGGGGACACCAGGGTACTTGTATCACC[T/C]CTCCCGCAACCCCAAGCAGCAGCAGCTTGCAGCTCCCAGGGAAAGACTCCTTCACTTCCACTTGGA
WI-1936	117	T	C	... AAAGAGGGACTTTGACACACAACTTGGA

Marker	Pos	A1	A2	Flanking	Sequence
WI-5204	54	C	T	...	TAGATTTTGATTGATGACAATAGGGAAGCCTTTGTTAAATTGGGTTTTTGAAGAA[C/T]GAAGAGAAAAATGGAAAGGGAAGGAAGAATTGACAGAAACCAAGAGAGTGTTGAGGGGCAGCAAATCCCAGTTTGACTGGAATATAGAGTGATGTCAGGGTTG
WI-5215	70	A	G	AGATAATTTGTAAAGATAGTTTTCGC	TTTCCCTTATTTATTTAGGAAGCAAAATGTTCATACAGGACCTTAATATTTAACAGACTCAAAAATAT[A/G]GCGAAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTAGCACATTTCCTGTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T	G	TTGTATCAAAGAGATGGGGTATATAA	CCCTGAAAATGTGCTTGCTTCCTCCCAACTCTCTAGGGAACTTTTTCCATGTCAGGTGGAACCATGTGAAGAGTACTTAATTAACTTGTATCAAAGAGATGGGGTATATAA[T/G]AAAGAACCATGTAAAGATTTGTTCTTT
WI-4456	49	C	T	AGTTGAATTATTCAGAAAATTTCCTGTTATTATAGTTCC	ACACATTTCATTTGCTTAAGTTGAATTATTCAGAAAATTATAGTTCC[C/T]CAAGTTCATGCATAACAGGAAACACCAGGTTGGGGCAATTGATTGAATTGT
WI-4461	49	A	G	TCACTGTTATTTTAAAATTATTTTGACCTTTCACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTAAAATTATCCTTCC[A/G]TGAAATTGGTGAAAGGTCAAAGAATGAAATTCCCACTTTATTGCGATGATAATGCAATGGGC
WI-4465b	75	G	A	...	CTACTGGATTTACTTTGCTCAAGCCAGACAACACGAAAGTATATAAAGAAAACAGTTAGTAATCTTTCACCTTT[G/A]TATTTCTTCTTCTTCTTACCTCAGGGAATC
WI-4465a	41	A	G	AAGCCAGACAACACGAAAGTGGTGAAAGATTACTAACTGTTTCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAGAAAACAGTTAGTAATCTTTCACCTTTGTATTTCTTCTTCTTCTTACCTCAGGGAATC
WI-1949b	160	T	C	GAGTGAATAAATGAATGCCATAATCTGAGAGGTGGGGACAAAAA	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCAGTGGTGAGATGCTCGAGTTCAAGGCTGCTGAGTCTGTGTTTT[T/C]CTGTGTTTTTGTCCCCCACCTTTCCCTGGCACA
WI-1949a	86	T	G	CAGTGGTGAGATGCTCTGAGTCCATGTCAGCAGCCTTG	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACACATAATGGCAGTGCTGACATGGTCATGGCTGAATATGTTGAAGAAATAAAGGAGTGAATAAATGAATGCCATAATCTGTGTTTTTGTCCCACCTCTCACACCTTTCCCTGGCACA
WI-4529	64	T	C	CCAAGTAAGTCTATCATTCTGAAGATGTTCTAAAAATAACACTTCCTGAAAAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTCTGAAGATG[T/C]GAGTTCTTCTTTATATCCTATGATTAATTTTTCAGGAAGTGTTATTTTAGAATAAACTCCTGGGTCCCATCCAGGTCTAGGGTCAATGGCATCGCTGCTGGACAAGATGGCATCCTAGGGATCATTTT

ID	Pos					Sequence
WI-4540	110	A	G	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTCCTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAACAGTACTTGCAATAAGCACCATGTGGCATCC[A/G]TGCAATGGCTGCTGCATTGTCCAGTC AAATGAGACAACTTCCTAT
WI-4582	226	T	C	---	---	AGCAAGCATCTGGCAAGCCTCGGTCAGGAACAGAACATTAAATTCACCAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTAACTTATTCCTGTACACA AATAACTTTATGGGAGGACAGCAGCATTGTAATTCAAATCAATAAATGACTCGGTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGT[T/C]CCTCCTTGCTAGAAACCATTTGAT
WI-1965	105	G	C	AG	GAATGGATGGG TCATCTCTCT	CAAAGGTTAGTTTAACTTGGGGGGCAAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGGAGTGTTTAAAG[G/C]AGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCATTTATTGGTGTGATGACAGT CATGG
WI-5248b	99	C	T	TTG	AGAAAAAGAG AAGAAGGGAA AAA	TGTTTAAAAACCATACAGTTGTGTCGTGTTGTAGAGCAACCCCAGAAAATTAAAACGCCTAC CATTTTTCACTGTTTCTATTGACCGTACTTG[C/T]TCTTGCTTTTTCTTCTCTCTTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38	G	C	CTACGTTGTT	TTTTAATTTC TGGGGTTGCT	TGTTTAAAAACCATACAGTTGTGCTACGTGTTA[G/C]AGCAACCCCAGAAAATTAAAACGCC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTTTCTTGCTTTTTCTCTCTTTTTCTG CCCTCTTTTAACTATT
WI-4596	69	T	A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTGCTCTGAAGCAGCAGAAAGCACTGTGA C[T/A]CATTATTAGGCCCCATCTCCTGCCTGAAGCCTGCCTACAGCAATTGTAACATATGGCATTGGGG ACATATCTCTGAGCCCATCAACTATTGACAAGAATTCTCCTTTTTAACAA
WI-5252	119	A	C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAATTAATACTGAATACCTGTGTGAATCATTGCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAAATAGTACTAAGAAAATATTGGGCCCT
WI-4606	61	A	G	GCAATGCTAG AAAATTATGC CT	TTAGGTGCTTA AGTGTCTACT TGG	CAATGAGAAGTTACCAGATGCGGGCAAAATTAAGCATATGAAAAATACCAAGTGTTGGCAGAGGCATG AAGCAAAGAGG[C/A]CTTTCATCTGCCCCGGTTTTCAGTAACTGCAACATGTCTTTGCCTCC ATTACCATTTATGGGGTAATTAAAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGTCTTTGCTATGCT
WI-5257	77	C	A	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG GCAAAT	CAATGAGAAGTTACCAGATGCGGGCAAAATTAAGCATATGAAAATACCAAGTGTTGGCAGAGGCATG AAGCAAAGAGG[C/A]CTTTCATCTGCCCCGGTTTTTCAGTAACTGCAACATGTCTTTGCCTCC ATTACCATTTATGGGGTAATTAAAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGTCTTTGCTATGCT
WI-4649	50	C	T	GAGACCATTCT TTCCGGAATG	TGTACTAGGTG TACTTACACAGA AATCATC	TCACTGTTTAGAAATTTCTTCTTCCTCAGTGAGCACCATTCTTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGTATTTTTTAA AAAAATCCTCCCAATATTG

ID	Pos						Sequence
WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT	GTCTCTT	G	CTGAAGTGTTA AACTGGATTTG G	AACTGTGTGGTATGTATTGTTTGTGTATTTTCTGGAGAGTCAGTTACTCTCCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTAATCCTAGAAGCACAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTGGAAAAAATTGTCCAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGGACTAGAACACAGCAGGTTTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGTCTATCATGAGGAATTCTGTAGAAAATTTCACCTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTCTTTCTTTGACGGAAGAAAACTTCAA[C/G][TCGAGAAAGGCTTAGATTATATCGCTGAAGCCCATTCTG
WI-4722	88	G	A	TGCACTATGG AACACCACAC	AATATGGAATC TGCATTCAGTT AAG	CTTCCCATTCTGCCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGAGATTTATTTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGGAAAATGGAGCCACATGTAACAGAGGAGAGCTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACTTTGATGGTTGAAGATTTCAGAAAAACGTGAAATTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAAACAGCAGTGTTGTCTAAAAAAATATGATAGTTTCTTCCTCCTGTCCACC GCAATGAAAGGAGTT
WI-2028	176	T	C	TGTTTACGTTC CCTGTCTCATC GAA	GGTTGGAAACT CAAATTACCTA	GACTACAGCGCCACGACAGAGGCATTGTGTGGCTTGCACAGGTGTTGGTTTGTTGTTAAGTTAGATT TGAATCCTTTAAAGAAGAAAGTGGCTCTTCAGTTACTACAGACCTCATCATCCTCGGTTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCTCATC[T/C]TTCTAGGTAATTTGAGTTCCAACC TGTGG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC A	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAATATAGTATTCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAATTTCCAAGGTTATACAGGACCAGTGTTGGAATTTT AGCATTCTGGGTTTGGCATCCATCAGGGTGCTAGAGAACTAATCCCTCA[T/C]GGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTTCTGGTGGAAGGACAAGAGTTGAAGCAAAAGGAGATCAACTGGG TAGAATAACTCATCGGATCCCACCAGCCTCCTTCCACCATTCTCCATCCTCCTACTTTCTACTCTGA[T/C] AGGCAGACTTATATGGAAAAAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	ACACTCTGAGTG	CCACGACTATGTCTTCAGAGTCCCTGTACTGACAGAGAAGGCTTGAGGACGAGGACCATGGCGCCAAGA CCTCCTTCTGCGGTTCAGTGAAAAGACGATGAACTCCTTCATCTTCTACAGCAGCTTCACCA CAGTGCACCAAGGAC[T/C]CGGACCTGCGACTGCACTCTATCTTCACCCCTTCCGACACCAGATGCTGAGATGCC ACACTCTGAGTG

Locus	Position	Allele 1	Allele 2	Sequence 1	Sequence 2	Sequence 3
WI-2038	155	C	T	TGTGCTTAAAGTGTGTAAGTATTAATTAG	ATTTCCTCTGAAAGAAACATCA	TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACCATTGTCTGTTATTGTCTCTTGCAGTGTATCCAAGGATGTCACTTTGGAACTCTGTAGATCAGAAAAACTGTGCTTAAAGTGTAAGTGTAAGTATTAATTAGATTTCTATTTGATA[C/T]TGATGTTTCTTCAAGAGGAAATTTGTGTAAGAGGATTCCCATTTGCATTCCATTGGC
WI-4782	113	C	T	GATGCAGAAGATAACTAGAAAATGC	GAACTCTTCTGGTTATTTTCTGTTC	TCATTGACTTTTAGAGTTCCTCAGTCTCTTATGTCTTATTTCTTAGGAAAAACTAGGCTAGGAGAACACAATTCAGGTCTCTCCAGATGCAGAAGATAACTAGAAAATGC[C/T]GAACAGAAAAATAACCAGAAGAGTCATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65	A	G	GCATAGAATCATCTTGCTAAGTTCC	GGATAAAATTAAAAATTTTGGCATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAATTCAGTGCATAGAATCATCTGCTAAGTTCC[A/G]TGAAAAAAATTATGCCAAAATTTAATTTATCCAAACTTAAGTCGAGATTATAATTGATATTTAAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T	C	TCCCAGAGACATTTCATAATCCAAAA	CTACTCTTCTCACTTCATTC	CTTACTTCCAAAGTGTTTTCCCAGAGACCACCTTCATTC[T/C]TTTTGGATTATGAAAATAGAAAGAGTAGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTGAGGCTCAGAGACAAGGTAGGTGATGAGCCCAAGGTCAGTGACAGAGCCA
WI-4818b	121	G	T	TGATAATGGGGCCCTGTT	CCTTCCTTTATATGTATGCCAGA	TATAATGTTTGTTCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATAATATAATTTATTCAAGAAGGAAAATATACATATGGGGTGATAATGGGGCCCTGTT[G/T]CTCTGGCATACATATAAAAAGGAAGGCTAA
WI-4818a	43	A	G	TTGCCATAGACTAGGTTATGTCG	CATATGTATATTTCCTCTGAATAAAATT	TATAATGTTTGTTCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAATCTTATATAATAATTTATTCAAGAAGGAAAATATACATATGGGGTGATAATGGGGCCCTGTTGCTCTGGCATACATATAAAAAGGAAGGCTAA
WI-5317	139	T	C	TTCCATTTCTGGTAGCAGGT	GATGCAAAGAAGAAATGAGTCC	TTTTCCATTTGTTGATTCTTTTGTCTGAGCCCTTAGATCTCCTTAAATTAATAGCAAGGTTAATAATATAATAATATGATGTTATATATTACAATTCAACAGGAATTCCATTCTGGTAGCAGGTATA[T/C]GGACTCATTTCTTCTTTGCATCTATTTCTAGGTTATTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G	A	GCAAGATATAAAGATTAAGAAAAGATAACA	CAATTCCACTACCTCATTTATTCA	AAATGAGTAACCCAAGTTACTCGGCAAGATATAAAGATTAAGAAAAGATAACAAGA[G/A]ATGAATAAATGAGGTAGTGGAAATTGCTTGATAACTGGAGTAGTGCCTT
WI-5328	44	A	G	---	---	AACATTTTTAACCATGCTACAGTTACAAACACTGAAAGAGACAG[A/G]AAAAAAAAGAATATTTGCCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAATATGAATCAGAAAGAGGAAAGAAATAGAAACACGTGATACTGGAGGAG
WI-4897	93	A	G	---	---	GCCTTTTTGAGTTAAGTCTTTTGAGTGGTGTCTTTTTTTCCCCCACTAGGTACTCTCGGCCCAAATCCCCAAAAGAAGAAAATAAGCGCCTTGG[A/G]GATAAAACACATCTTC
WI-5345	29	G	A	---	---	CCCTGCTATAGGTCAGTTTTAAAAATCCT[G/A]CCTGCTATGGTTTGCTTGTTGAAGCCACATCCACTGAGGTATATTCTGTCTGCATTTCTATATCACTCAGCTTCAGATCCATCCATCAACTTGCAG

Clone	Pos					Sequence
WI-5370	143	T	C	AATAAGATGG TACCTTAACTA ATAAAAACAA	CAAAGTTGGTA CAGAGAATTTC AAA	TGCATGTGTTACTTCTTGGAAATCATAAAGGGATCTGAGAGCCTACAGTGTATATGGCAACATTAACCAAT CTTTTGAAAATTTACCTGTATCCCATCATGGTTACCCATGGTTACCCAACTTTGCTTTTC ATAAAACAA[T/C]TTGAAATTCTCTGTACCAACTTTGCTTTTC
WI-9711b	423	T	A	---	---	GATCTCCTTCATCCCTCTCCAGAGAGGAGAAGAGGAAACACAAGAGAAACGCCTGGTGCGGGGAAAGCAC CCAATTCCTACTTCACTGGATGTGAAATGCCCAGGTGAGGAGACGGCTCGTGTATCCTTGAAGCTGTGCAGCTT TGGACCTCAACAGTTGGAAAATGTTGTAGTGTTAGCTGTCTCGTATCCTGATACTCTTAAAATTTGAATG
WI-9711a	390	C	A	---	---	CAGTTTCTTCGCCTGTGGAAAATATTTCCCTGATACTCTTAAAATTTGAATG GGAGGAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTGTGTGCCTATTCAGCAATTCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTGACTT
WI-9702c	345	G	A	---	---	TTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTGATAG GGAGGAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTGACTT
WI-9702b	344	C	T	---	---	TTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTG GGAGGAAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCCTCTGTGCCTATTCAGCAATTCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTTATT[C/T]TAACTTTAATGATCTCTGTGA CTTTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTG
WI-9702a	179	C	T	---	---	TATAGTATTTAACGAAGCCTAGAAGCACGGCTGTGGGGTGATTTGGT[C/A]AGCATATCTTAGGT ATATAATAAACTTTGAAGCCATAACTTTAACTGGAGTGGTTGATTTCTTTTTTATTTATTTGGGA GGGTTTGGATTTTAACTTTTAACTGTTGTAAATATTAAGTTTTTGTAAAGGAAAACCATCTCTG TGATTACCTCTCAATCTATTGT
TIGR-A003N21	49	C	A	---	---	AGAATGGCTACTTCATAGGGCAGGAGCAGCCACTTTGGCTAATTTTAACATCCAAAGCTAATAAAT AATCAAGAAGAAATAGAGAACATTAACAAAATAAAATTATGTTCTATTTGGGAATACCTAATATCAG ATACTAACAAGTAGCAGTGATAAGAATAAAAAAGATAAATAATCACACATACCTTCTAGGTTAGTAGA
TIGR-A004V30	203	C	T	G	---	AAAG[C/G,T]CTTCTAGGTTAGTAGAGAAAAGTT

Name	Pos	A1	A2			Sequence
TIGR-A004W22	232	C	A	---		GGATAAATCAGTACAATAATGGGGACCTTAAAACTGCTGTGATGCAGGAGGTGGGAGGGCTGGGCAGTGCCCGGAGGCAGGGAGGAGGACAGTGGGACAAGGGATGCTCAGTGGTGGTCAGCAGCAGGGGCCTGTGAGTCCAGAGCAGTGGGGCATGGGAATGACGACCAGGTTCCCACATCATGCACGCCCCCGCGCCTA[C/A]CTGGAGATGTCTCTAAAAGCCTGCCCACATTGGTGCTGCCCAC
TIGR-A005D24 b	138	C	T	---		CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCTCTTTGAGATAATTGATTTCATATTCTGTGGCTTCAACCTCCATTTACCTCTTGTCATTCCAACATCTTTATAGAGAAATAAAAACCCAATTTCT[C/T]TTTCACCATTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATTGTTATGTAAATTCATAAAACTCCTTCACCTTTAATAATTAAGGAAACAAT
TIGR-A005D24 a	123	A	G	---		CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCTCTTTGAGATAATTGATTTCATATTCTGTGGCTTCAACCTCCATTTACCTCTTGTCATTCCAACATCTTTATAGAGAAAT[A/G]AAAACCCAATTTCTCTTTCACCATTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATTGTTATGTAAATTCATAAAACTCCTTCACCTTTAATAATTAAGGAAACAAT
U03735	74	C	G	---		TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGGTCTGGGCCAGTGCCACCTTCCGGGGCCGCATCC[C/G]TTAGTTCCACTGCCTCCTGTGACGTGAGCCCATTCTCACTCTTGAAGCGGAGCAGTCAGCATTCTTAGTAGTGGGTTTCTGTCTGTTGGATGACTTTGAGATTATTCTTGTTCCTGTTGGAGTTGTTCAAATGTCCTTTAA
U39840b	42	T	C	---		GGTTTGTCTGGCATAGCCATGCCTGGTAGCAAGAGAGAGAAAAATCAACAGCAAACAA[T/C]CAACAGCAAAACAAACCACACAAACCAAACCGTCAACAGCATAATAAAAATCCAACAACTATTTTCATTTCATGCAACCTTGCCCCCAGTGCAAAGACTGTTACTTATTATTGTATATTACAAATTCATTGTGTATTACTACAAAGACGGCCCCAAACCAATTTTTTCC
U39840	56	A	C	---		GGTTTGTCTGGCATAGCCATGCCTGGTAGCAAGAGAGAGAAAAATCAACAGCAATAAAAATCCAACAACTATTTTCATTTCATGCAACCCAAACCAAACCGTCAACAGCATAATAAAAATCCAACAACTGTTACTTATTATTGTATATTACAAATTCATTGTGTATTACTACAAAGACGGCCCCAAACCAATTTTTCC[G/A]TGAGCACTGCTACAAACATCCA
WI-8997	41	G	A	GCCCACTTGCT CCCC	TGTTTGTACGC AGTGCTCA	TATACCACTTCCATTTGATGATGAATGCTGCTGTTCATGACCAACTTTATGGCTAGATGGGTCAGAAAGCACCCAGTCAGTTCATGATAGGCAGTCAGGTCATATGGTCAGACTTGATGACCAGAGTCAAACATTCAG
WI-7008	180	A	G	---		TTTCCACCAAAGCCCAGTAACAGCCCAAGAGCTGTCTCTCAAAAG[A/G]AGAGTAGTTATCTGCAGAAGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACCGGCACTGTGATTCACCT
WI-9005	26	C	T	CGAATTTGCTG GGGAATCT	TCCCAAAAGTC TTAAGAAGAA AAA	GGTCCCACGAATTTGCTGGGGAATCTC[C/T]GTTTTCTTCTTAAGACTTTTGGGGACATGGTTTGACTCCCGAACATCACCGACGCGGTCCTCGTTTTTCTGTTTTCTGGGGTGG

Marker	Pos			Flanking	Sequence
WI-7593	46	G	A	---	TTTTTGTTGCTCTGGACACCCACTGCTCCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTTTTGGACACTTCCTCTCTTGAAATATAAAGAATCAACAAGTTACAGTCATGTTGGGGACTTCTCTCTCCAA
WI-6962	78	A	G	---	AGTTGCATCTTGGGGGAAAGGGCTCCAGTGTTATCTGGACAGTTCCTTCATTTCAGGTGGGGACTCTTGATCCAGAGA[A/G]GACAAAGCTCCTCAGTGAGCTGGTGTATAATCCAAGACAGAACCAAGTCTCCTGACTCCTGGCCTTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTTAGATAAGA CTATTCTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTTAGATAAGA
WI-7059	43	C	G	AAGGCACCCAGCCATC GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAAGGCACCCAGCCATC[C/G]TGACCCAGCCAGCGAGGAGCCAACTATCCCAAATATACCTGGGTGAAATATACCAAATTCTGCATCTCCAGGAGGAAAAATAAGAAATAAAGATGAATTGTTGCAACTCTTAAAAAAA
WI-9063	53	A	C	CACTTCACTGAAAGACACCAT TT TCTACTTCTGCCCTTGGGT	AGCAGCCATCACACTGATCTGTTTTTCACCACTTCACTGAAAGACACCATTTAT[A/C]TACCCAAGGGCAGAAAGTAGAACTTACTATTCATTAAATGTTGACACAATTGGAATTGTC
WI-7079	293	T	G	---	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCCACATACCATCTGTAGAGTTGGAACTGCATTCTTTAAAGTTTATATGCATATATTTAGGGCTGCTAGACTTACTTTCCTATTTTTCCATTGCTTATTCTTGAGCACAAAATGATAATCAATTATACATTATACATCACCTTTTGACTTTTCCAAGCCCTTTTTACAGTCTCTTGGCATTTCCTGCCTAGCCCTGTGTGAGGTAACTGGGAT
WI-9074	38	A	G	GGTAAAAGTTCTTTTGCTCTAAAAG GACAGATTTTGACCTAGTTCCTT	TGGATGCCGAGGTAAAAGTTCTTTTGCTCTAAAAGAA[A/G]AAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGCAAATGTAACTGT
WI-7104b	249	C	T	---	GGAGTTTGCCCCTTCCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGAGAAGAGAGAGAGTGCCAGGAGACCCTGAGGCAGCCCGGTTCCACTTTGGACTGAGAGAAGGGAGCCCCAGGCTGGAGCAGCAGAGGC[C/A]CAGCAAGAGAAGGGCTTGGGTTCTGAGGAAGCAGATGTTCATGCTGTGTGAGGGCCTTGCACCAGGTGGGGGCCACCAGTCTTTG[C/T]T
WI-7104	157	C	A	---	CATACAATGAGAGCCCTGAGCCCTCAGAAGAACTCA[C/T]GCCAGCTCCAGCCCTACACCAGTTTCCACCTGGAGTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTTAA
WI-8974	34	C	T	CCTGAGCCCTC TGTAGGGCTGA AAGAACTCA GCTGGC / GCTTACAGGAG CCTAAGCATTG AGACTAGACA CCTGGC GGAA	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC[C/T]TTCCTGTCTAGTCTCTCGTGTAAGCCAAAGAAATGAACATTCCA
WI-9161	61	C	T	---	CCCTGTTCCCATCTCTGTCTGTTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGCTGGAT
WI-9014c	93	T	C	---	GTCTCCATCTCTGTCTCAACTTTA[T/C]GTGCACTGAGCTGCAACTTCT

ID	Pos					Sequence
WI-9014b	44	C	T	...		CCCTGTTCCGCCATGCTGACCTGTGTGTTCCTCCCCAGTCATCTTTC[C/T]TGTTCCAGAGAGAGGTGGGGGCTG GATGTCTCCATCTCTGTCTCCAACTTTATGTGCACTGAGCTGCAAACTTCT
WI-7023b	206	C	A	...		TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTGGTTTGTGACAGACCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCCGCTGCTGACTTGAGTGGGATCAACATCTGTCCTTCCCATTCAACAC TCTTTTTTGGCCCCAGTATTCATGCTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA A[C/A]ACACACACATTCTTGCTCTCA
WI-7023a	56	A	C	...		TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTCATGGGTTTGTGACAG[A/C]CCCTGCGT GCTCAGTGCCCTTTAAGTGCTCATCCCGCTGCTGACTTGAGTGGGATCAACATCTGTCCTACGGGTC CCCTCTTTTTGGCCCCAGTATTCATGGCCAGGGGTTTGTTGGACACCTAGCTTCCCCATTCAA CACACACACACACATTCTTGCTCTCACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54	C	T	...		CTGAAATCCCCTCTCTGCCCTGGCTGCCGATCCGGGGACCCCTTTGCCCTTCCCT[C/T]GGCTCCCAGCC CTACAGACTTGCTGTCTGACCTCAGGCCAGTGTGCCGACCTCTCTGGGCCTCAGTTTTCCCAGCTATG AAAACAGTCATCTCACAAAGTTGTGTGAAGCAGAAGAAAGTGAGGAAGGCCGTGGGCCAAT GGGAGAGCTCTTGTTATTATTAATTATGTTGCCGCTGTTGTTGTTGTTA
WI-9171	62	G	A	...		ACATATCTGAAAAATGTTGAAAAGCTAAGCCAGGAATAAAAGAAAGTAGAGAATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAGCTTGTATTCACAAGACTTCATGC
WI-9174	47	T	C	CTAGGACCCC ATTCTCCTATT CT	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATTCTCCTATTA[T/C]CAGTCCTGTCCTATATA CCCTCTAGAAACAGAAAGCAATTTTTAGGCAGCTATGGTCAAATTGAG
WI-7753	52	A	G	CCATGTTCCGA GAAGAACAGA A	CAGAGGTCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGACATCCCATGTCCGAGAAGAACAGATA[A/G]ATCCCTGTATT TCAAGACCTCTGTGCACTTATTATGAACCTGCCCTGCTCCCCACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76	G	A	CCACTTCTCCC CGCA	AAAGGGAAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAAACAAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGGTCAGACTTTCCCTTTCATCTT
WI-9193	94	G	A	AGAATATTGT CTGCCTTAAAG CA	GGTGTGTGTGG TAGGGGG	TTGGACAAACCTAGAATTTCTCCCTTTATGTGTATCTCTATCGATTGTGTAGCAATTGACAGAGAATAA CTCAGAATATTGTCTGCCTTAAAGCA[G/A]TACCCCCCTACCACACACCACCCCTGTCTC
WI-9015	48	C	T	...		TTTGGATTGATATCGTGAAATAAACACAAAATCCATTCCAGGTATCGGCACCAACTAAGAA CTTTCCCTAAAGAAGAATAAAACACAAAATCCATTCCAGTGAGCTGGCACCAACTAAGAA
WI-7254	37	A	G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGGAGACAGGGTCTGAGAGGAGCCAC[A/G]GTCCCTAATGACACCCACTCCTAGCC CTGAGGCTGCTGCGTGCCCCTCAGACTGGGGAAGAGTCCAAGGAAGGGAGGAGCAGCCACTCCTCAATGC TCAATGGCTCCCCTGAAATCAAGACAGG

ID	Pos.	Alleles	Flanking	Sequence
WI-9231	32	G C	CAGGTCCCCCA GATTGA / CACTTGCCCAC ACTCAGAC	GTGACCCTGTGAGGTCAGGTCCCCAGATTGA[G/C]GTCTGAGTGTGGGCAAGGTGTGTCAAAAGGGGC TGCCCCCAGGAGGATGAGCGTGAGAGCGGGAGTTGAGGCCGAAGAAGTCA
WI-7836	120	T C	CAAATAAACA ATGCAACGTTC C / GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAAATGTCATGGTCTATAACTCCAAATAAACAATGCAACGTTCC[T/C]GATTTCTAAT CTTGGTTCTGAGAGCCATTGGTTCAGTTGTAGCAATCCCCATACCAGCT
WI-7286	65	T C	CAGCTTCAGCT TAACTGACAG A / AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCCTTTGGCCCCTGCAGCATGTCATGCTCCCAGAATTTCAGCTTCAGCTTAACTGACAGA[T/C] GTTAAAGCTTTCTGGTTAGAATTGTTTCCATGGTGATCATCGTCTTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91	T G	CTAAGCATGT ACGTGAATTTT TAAAT / CCCAATTTTTA TTAAAAGTTTA CATCTAT	CAAATTCTTGGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAAT[U/G]TATAGATGTAAACTTTAATAAAAATTGGGGTGTGG
WI-7860	50	C G	A	GAAGATTAAGGGAGGGTGTGCTCTGTGGTCTCCTCCCCTGCCCTCTCCCCA[C/A,G]TGGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCTGGCCTTATGGTTGGGGGTGGTAGGCAGG TGAGCGTAAGTGGGGAGGGAAATGGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTCAGACCAG ACCTAGGTGCTTCTCTAGGAGGGAAACAGGGAGACCTGGGGTCCTGTGGAT
WI-9064	29	A G	CGTACCTCCAA ACATAATTGA TTC / GCTTGAGTGTA AGTCTCGCAGA	CAAGGGCGTACCTCCAAACATAATTGATTC[A/G]TATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGAGGCGCCTGCTACTGTCTCTCTGCTACTTTG CACACTTGTCTGTTCTTCAGTGCTGCGAGGTCTGGCAGGGGTCTGGGGTAAGCCGGGGGTTCCACA GGGCCCAGCCCTGCGCAGGGGTCTGGCCCCCAGGTAGGCGGGAGCAGTCCCTCCCCTCAG[G/T]AACT GGAGGAGGGGACTCCAGGAAGTGCAGACCACCATCCTGAAGCCAGCTTGCACCTCCAGT TTGCACAGGGATTTGTCCTGGGGGCTGGGGGGTCCCACCCCCGCCC
WI-7307	128	G T	GAAATGTGAC TTCACTTGGT G	GAGGAAATGTGACTTCACTTGGTG[C/T]CAATGGACAGAAAATTCTACCTGTGCTACATAGGAGAA GTTTGGGAATGCACTTAATAGCTGGTTTTTACACCTTGGTTTTACACACTTGAGTGGTGGAAA
WI-9274	25	C T	CAGGTAGAATT TTCTGTCCATT G	AATTCCTTTCTGGTAATCAGGCACATGATGAACTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTGCAGTCTTTATGTTTATTATCATAGGTGTAGGTGGACCTAAATTCCTTATCATATCTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTTTTATGTTTTAAACTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTTAAACTGAATTGTATAGCGATGA
WI-7313e	266	T C		AATTCCTTTCTGGTAATCAGGCACATGATGAACTTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTGCAGTCTTTATGTTTATTATCATAGGTGGACCTAAATTCCTTATCATATCTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTTTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTTAAACTGAATTGTATAGCGATGA
WI-7313c	256	C T		

ID	Pos						Sequence
WI-9281	68	G	A	...			ACTGGTGGGAGACTGTGAGGATCCCAGGATTCAGTATTCCTGGCCATGCCTTGCTGCTACTGG[G/A]TGTTAGTTGCAGTCCTGTGTGCTTCCCTCTCTTATGACTGTGTCCC
WI-7848	142	A	G	CTC	GCTAACACTTG TTAAAACCGT GACA	CATTTATTTG AAAGCTATTCA	TTCTGAAAATATAACCAGCCATTGAGCTATTTAAAACTTGTAATTTTTAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAAACATTAATGCTAACACTTTTAAA ACCGTCTC[A/G]TGTCTGAATAGCTTTCAAAATAAATGTGAAATGGT
WI-9304	70	G	A	ACTGA	GTATATTACA ATGATCACCG	CCCCACAGAAC TATTGTAAAAC AA	TCACGTTTGGTGCTTCTCAGATTTCTGAGGAAATTGCTTTGTATTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCGTGTGGGCTGTTTTTTGT
WI-7933b	314	C	A	...			TTACAGAAACTTGCCCTGTGCCTGTCCCCCATGCTAGGGGCGGAGGGGTCTTTCCTTCTTCTTTCC TACCTACCCCTTTCTCTTGGCCAGGGGCCTCGTATCCTACCTTCCTTGTCCCCTGGGCTGGCTGCAC AGAGGATTGCCCCTCTCTTTCAGAGCTGCCCTCGATGCCAAATTAGCATTAGTATTTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCTGGGGAGGAACCATAGCTCCCT
WI-7933	96	G	C	...			TTACAGAAACTTGCCCTGTGCCTGTCCCCCATGCTAGGGGCGGAGGGGTCTTTCCTTCTTCTTTCC TACCTACCCCTTTCTCTTGGCCAGGG[G/C]CCTCGTATCCTACCTTCCTTGTCCCCTGGGCTGGCTG CACAGAGGATTGCCCCCTCTCTTTCAGAGCTGCCCTCGATGCCAAATTAGCATTAGTATTTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCTGGGGAGGAACCATAGCT
WI-7374	182	T	A	...			CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTTGACTTTGTTAAATATTTGAAATGTAAATGAAAAGAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTTCTAGCTGCTGTTGAAGAATATATTG[T/A]CAGAAACACAAGGCTT GAT
WI-9343	78	C	T	CCAACAACAT CCTCTGCCA	AAAATGAAACTT ACGTTTTGTTG TG	GGTCTGCTGCTGGACCCTTCCCTTTCTCTGCTTCTCTCTCATCATCATCCCAACAACAT CCTCTGCCA[C/T]ACACAAACAAAAACGTAAGTTTCATTGGGCAAA
WI-7386b	104	T	A	...			CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTCAACTCT TAAAGACATCTTAATCCTGAAGTAAACAACAATTGTTA[T/A]GTGTTTAGAATCAGAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A	G	...			AAGAAGGAGCTCAGTTACGGGGTTTTAAAACCTTCATGAAAACCTGAAGAGTTCACTTTGTTATTAT GCTCTTA[A/G]TGATTTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79	T	C	CTTTAGAAAAA TCTGCTTTAAC C TTGG	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGG[T/C]ATTCCTCTAATTGTGTTCCCTAGGAAATGAACTGACTGTCCCAAG
WI-7423	107	T	C	TGCTGGGCTGT GTTCC	GGTCCAGAAGA GCCCG	TGCTCCCGTGTCCCCATCTCGCAGTGGACCCCAGGCACCCCCTTTGAGGAGTTGGGGTGAACTGCTCCTT GATACCAGGCCATGTGCCAATGTGGTATTGGGTCCTGGGAGGTGGGTGAAATAAAGGCATACTGTCT

	CAAGAGAGAG AGAGGAAAGA A AAAA	TGCAAAGAAA GAATGAAAGT G		CCAGGAGCACTAGAGAGGGAGGGGGAAGAGCAGAAGTTAGAGAAAAAAGGCCACGGAGGAAAGG
WI-7424	131	T	A	AAAAAACATCGGCCAACCTAGAAACGTTTCATTCGTCATTCCAGAGAGAGAGAGAGAAGAAAAA [T/A]ACAACTTTCATTCTTCTTGCACGTTCATAAACATTCTACATA
				TCCTGCAAGAAGTTCTCAAGCCTTTTGATTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTCTTCTTAATTTAAGTGAGA[A/C]TCTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAAATCTAAAATTATGTACCACTCGTTTATTTGTTCATTCATCCA TCCCTTTCCCATGAATATTCA
X86400	118	A	C	GTGGCCACTACATGTTATAGAAACCATCATCTTGTCACACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAGAAAAAGCATTAAAAGTGTCCCATTAAAAGGGACTTTAATCAACCTAA TAAACTCTAATTCTGCTGACTTTTAAAGATCTAAGGTCATTTAATACATGCTGAAAAGGGTCACA ATTAATTCTTGATCTTTTTACTCACTGTTAACTTATATAA[T/A]TTCAGAAC
WI-8053	242	T	A	TACACAATGAATTGCTTTTATTTCGGTATGCATCCACATTTCAGCATTTAGTGGTCCTGAACAGCAAG TGGAAAGAGACGCAGCAATTTGCCAGGAGGTCAAGCCCAACCAATTTCGGGGATCTGCTGTGCACCGG GTTCCTTCTAATCCCTGCTGAGGATCTTG[G/A]GAAGCAGCAGCACCAAAACCAAGGCATGCA CCGGATTCAAGGTGTCTTTTTGTTCCAGTTGTGTCAGATTCCAAACTAGACCCCA
WI-6190	165	G	A	AACAGTCACCACCAACCACATGACAACTCGCCCAGGCAAGGCCTTGCTTCCCTCCCTCCTTTGCGTCCC ATGTGTCCAGTCAGCAAGGTCGGGGAGGCACCGATGTTAGCTTCGGCCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAAA[G/C]GGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAAATCACTTAAAACTG ATTTGCTTTCAGTAACTGGTATGTCTGAA
WI-6275	148	G	C	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTTGATTGT[G/T]GGGCTTCCTGAAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGAACCGTACCTGAGAGGGATGGGGCTCTCTCACAAAA GAATATTTGGGGCAGAACCCTGGAACTGGCCACCAGGGACATCCCAAATATCCCTCCTCCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAAGGCTCTGAA
WI-6421	41	G	T	GGGTGAGACGGGTTTATTGTGCACATTTACACAGCGTCGGGGCTGGCAGCGGCCATGCTC CTGTGGTCGGGCTGCTCTACAAGGGCGTTCACTTTTCTTCACCACACTATGTACAGTGCTCCAA GGTGATGGGCTACAGTGCTGCGATCAGTGAGTCTGTGTACACACATTTTACATAAATTACACGACTC ATACATGAAAAAT[T/A]AGAGCCTAAGGGCCTGTATTTTAATGAGAAAAAAA
WI-6905	215	T	A	AACTTGTTTACAAAATAGGCTTTGCAAACTTCATTACTGAATTGTAAAGTCAATGACTGTGTTGTTTT TAAAATATGTACCAAGGAAAATACAAATTGGATAATGATCATTTTCATGCTCAGGAGGAACAGCAC AGAAAATAAAGGATACTGCACAAGGTGCAAGGAAAACCGGAACCCATTGTACACTGTTCTTCACACAG
WI-9420	202	G	A	[G/A]GCATTCTTTCTCACCTTAACTGCAGCTGTGCAAGATGCTCAGTGTG

Marker	Pos			Sequence
WI-9448	184	G	A	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGGAGAGAGACTGCCTTGCCCATGGTGGTTAAAACTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCCTTTTAAGAAAAATGGCTTGTGGTTCCAAGCGCATGTTCCTAACGTGCCCGTGAGCAGCACCAC[G/A]CACTGGTTTCTAAATCTCTGGCTTGGATTTTATCCAAG
WI-9470	204	G	A	ATGTCAGAGAGACACAGACAAGAGGAGTTTTTCCCTTTAAATGCTAAACAAGTGCCACTAATCCACAGATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCCAGGCTTTTCTTGTCAGTCCGCTTATGAGATCACGAATATGATCTCCCTAAAGCCCAGATTCCTACTAGAGCCGCTGGGGACACTGATGACAA[G/A]GCAATCAACTCATCTCTCCAAGCTCACCAGGGCTCACCTTCCCAAG
WI-1245b	201	G	T	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCATCCTAGGGCAATGGTAGGTGCCTGATGCGAGATCGTGCTGTGAGCCATGTCGTGGCATCACAGGGGTTATTAATTCATTTATCATCTGGACAGCCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGCGCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAAT]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T	C	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCATCCTAGGGCAATGGTAGGT[t/c]GCCTGATGCGAGATCGTGCTGTGAGCCATGTCGTGGCATCACAGGGGTTATTAATTTCATTTATCATCTGGACAGCCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGCGCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G	A	TTCAGTGATAAGGACAGGTCTAGAAACAAGGCGTTCCCAACCCTGGCACCAATGACAGTTTGGACCAAATAACTCTTTGTTTCAGGGGGATGTTCCTACACATTGTGGGGATGTTCCTACGGCCTCCGTGGCCTTCTACCCACTAGATGCCAGCA[g/a]CACAACACCCCTCCCCAACATCATGACAATGAAAAATGTCTTTAGACATTGCCAAATATACCTTGTGTGGGACAAAATGGCCCCTGATTGAGAACCACTGGTT
WI-5385	110	G	A	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAGAAATGGTGACTCCAATGGTGGATTGAAGAGGGAAGTCTCGATAATTTTAACATATGGTTTCTTGCCAGGAATCG[g/a]CAATGCTAATCTATTGCTAATTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGAGTTCCTGACCCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T	G	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCACCCCAACTTGGTCGTTACCCTATGCCGGGGTGGGATTGAAGAAATAACCATAAATAATAAGTACAATTTTCCAGTAGTTACCAGGCACCAGCCTATTGGAAGAAATCATAAAGTGTAACCCTACAAATGTATTGCTCTCTGGCTTGGTGCCAGGCATAGAGTT[T/G]GGGCCTACAACCCATTTTATCATTGAACCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G	A	TGGTATTTTCCTTTTCCTAAAATGTTATGATTAATTAGTGTCTTTGTAGAAATTGAAAAAATGTAAATCAGAGAACAGAAAGAAAATAAAGTAAGTATAGTTGAACCTCTAACAATTTAGATTTTAAGGCCTAGGGAAAGAAAAGAAGAGCCTGGAA[G/A]AGGGAATGAAGAGAAAGCACAACCAGAAAAAAAGTGTGTGGCCTTAAGGGGAAGCCAAGGAAAGTTAAGT

ID	Pos			Sequence
WI-5801a	48	A	G	TGGTATTTTCCTTTCCTAAAATGTTATGATTAATTAGTGTCTTGT[A/G]GAATTTGAAAAAATGT AAATCAGAGAACAGAAGAAATAAAGTATAGTTGAAACCTCTAACAATTTGAATTTTAAGGCC TAGGGAAAGAAAGAAAGAGCCTGGGAATGAGAAAGCACAACCAGAAAAAAAGTGTGT GGCTTAAGGGAAGCCAAGGAAAGTTAAGT
WI-5696	61	C	A	TTCTATTTAAATCCTGTGCCCCATTCAGTCTGCAAGACTGCATTCAGTCTGCGATGAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCACACCGAGGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTCTCTGTATTA TACAAACTGGGACCAAAGATGACTTTATAATAGTGCAAGAGACAATCAGGCAGGACTGGGAGGACC TTATAAAATAGATTATATAAGGCTGTGGTGAGTTTATTTTAACTT
WI-7461	153	C	T	TATTACTAGGTTCATAGAGCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCCC AATTCTAACGCTCCTCACTTCCCTTCGAACCTAGGCTTGCACATTCCCTG TGGGCAGGGACTGGTGTC[C/T]GTTCCCTGTTGGGTCCCCTGGCCACAGAG GAGGCCCTGAGTAGCAGTGTCTGCA
WI-9716	221	G	A	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTAATGGTCCCTTGTCTCTAAC GCTTTTGGTATACTTTCTCTTTCTGAAGACCAACCCTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCCTACATTCTGGAAAACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAATTCTAGAA[G/A]AAAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49	C	T	TTTTCGTTAAGTCTGTGAAGCCACACAGAAGTGATCTACTCCTTTAC[C/T]AAGTGTTACTTTGCA TATATTTTATGGGGATGATTCTATCCCTACTTAAGATTTCTCTTCTCCAGGTAAATATTCCATTCCT TGTTCAGGAGTTTCTTATTGGCCTTCTTCTAAACCCTTAACCATTCTGCTTATTCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A	C	GAAAACCTCGTTGGCTCAAAGGAAAACTGTAG[A/C]AAATTCTCTTTTTTTATTTTGTTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGATGGCCACGCTGCTCTTCTTTTGTTTTGGTGTAAATCCTCTAGT GGGCACTTTGCAAAAGCAATTTTAGAGCAAAGGTGGTGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAAATGGAAGAAAAGGTAATGGA
WI-10312	41	A	G	AAGGCCCCAGTGTGGGAAAAAGCAGAACAAACACTCCAAGAATAC[A/G]AGATATAAAAACATCATCATCA GTAGAGATGGGGATGACCTAGGAGGTCATGCTGATGGAGGCATGTCAGACCAAAAGACATTTGGGTCT TGAGGGGTTGAATAGGAGTTTGTCTGGTGAGTCTTGCCCAGTCCCATAGTAGGTTGTCCATAAATAAAC AGTGACTAAACTGAGGTAGAGTCACAGAGAAGAAAATTTCA
WI-11152	179	C	T	GATTCTTTGCGACATGCGACGAGCAGGCAGATACGGCAAGGCATCTTGGGAAGGAAAGCGAGCCCTA ATTCATAGAACAGACTCTACAAAGGACACCAGTTAGGAGAGAGGCTCGCGACCAGGGGACTGGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAAGGCTTGTCA[C/T]TGTGTCAGAAACAATTGAA AACAGCCAGTACATGCCACTGATAGA

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WI-1968	167	A	G	TGGTGAGGAGCTGTAAGGCTGAAAGAATAGTCTCTGCTCGTCTGTGGTCTTTCGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCCTCTGCCATGGGTGTTTATGTTGTTAGAATCATGGAGTTGGAAGACTTAGAATTCA ATTTGGGGCTGTACAGTTGACTGGAAGTTGT[A/G]TGAACTTGAGCAAGTGTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198	G	A	GGGTTCATTTAACAGCCTTCCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAAACAACAACAACAACTAAACTCCTCCCCACTCTA CCCGCCAAAGTCTACCTTTGGTTCTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164	C	A	TTTATCTTTCCAAACCATGTGTGTTTTCTTCACATACTTTACGTAATTTAAATCATGTCATTTAATTA TGCACTTACTTGTTGGCTACCAGACATTGCTTCCAATTGTAAATTCCCTAACACAGCCAAGCATAACT GATGTGTCCATCTTTGTATTCCTAAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCCTCTGT CTTCCTCTGTTCACCTCCTGTATTCCTGTATTCCAGCATTCAATGATTA
WI-4860	72	A	G	AAAAAAACAACTTCATTTGACATTCTAAGAAGAAAACAACGATCCACTGTGTGTTTGCTT GATTT[A/G]GGAGATAAAACCTGATCTCTAAGAAAAATTAAACCAAGTACACTAAAATAGCCT TTGTGTGTGGTTTTCAGGAAAGAAAGCCAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAATATAGCA
WI-9705	111	C	A	TGAAAGGACCAGTTCGAATGCCTACCAAGGTAAAGTAAATCGGAGGGCAGGAAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAATTGTTAACACTGATGC TGTCTACAAAACGCACATAGAAATCGGTGGTAGAATTGCGGTTCCTAGTAAGTAGCTAATGTTTAGATA TGATTGTGAATTATTGTTGCTGTGTCTTGGTG
TIGR-A004Z48	177	A	G	CAAAATAATCTCTGCTTAGAAGTTGCTCTAGGCCCATGGATTCATGTGTAAGGGTGGGCAGGGTGGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGGTGAGGGGGAGAGATCGTGGGTTCATGAGATCCCAT CTTGGGCAATACGGGTTATCCCGTGGTCTTCATACGCCACAGA[A/G]TCCTCCAATTCAGGGGGCTCCC GTGGGGATGGGTGGAGCCAATGAAGAACCAGGTAGATGATCGCCACCTAGAGATG
U17579	34	T	G	GGGGATTCAATGTGTCTGTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTCTTCCC TATGTTCCCAGAGAACAGAGAATAGACCTGGCCCCCTTCCTCTAGGGGATCCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTCGTCTGGGATCAATTTCTATGGGAGCC TGGGGAGAGGGATCCTTTCTAGTTGA
WI-7747b	88	T	G	GTGAGAGCGGAGGCTGAGCCTACAGATGAACTCTTTCTGCCTGCCTTTCGTTAACTGTGTATGTACATA TATATATTTTTAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTGTTTGTTTGGGTATCCTGCCCAGTGTTGTTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCACCATTTGTAATAAAGTATATAATTTTTATGTTTGTTTCTGA

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WI-7747a	44	T/C	GTGAGAGGCGAGGCTGAGCCTACAGATGAACTCTTCTTCTGGCCTGC[T/C]TTCGTTAACTGTGTATGTAC ATATATATTTTTGTTGTTTAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTGTTTGTTGTTTGGGTATCCTGCCCAGTGTTGTTTGTTAAATAATTTTTATGTTTTGTTTCTGA GTTTACCATTTGTAATAAAGTATATAATTTTTATGTTTTGTTTCTGA
WI-7189	197	T/C	TCCAGAATTTTCCTTCTTCAGCTCATTTTGTCTCTCTCACAATTAAGGGAGTTAAGTGAAAGGT CACATACCATTATTTCCCCTTCAAACAAATAATATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAACTGGTGAAAATTACCTAAAACCTT[T/C]AG TTTGCAAATAGAACTAATACTGGTGAAAATTACCTAAAACCTTGGTTATT
WI-7850	57	G/A	AGCCCCAGCTGGACTCATGGATGTGCACCCTTGCTCCCTGCTCTTCTGCCTCTGG[G/A]CTCATGTA TCTGCGGCAGCTCTGGTACCCTGTGTGGGTGCCATCTCACCTCTGACACAGACTGCCTGCCTTGAAGCT GAGAAGGCACAGGGCCAAGGAGCCACAGAGCCTCAGCCAGCCCAGGATCCGTCCTCCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGCGTGTCTACTAGAGCC
WI-7907	69	G/C	CTCTTCTTCATCCCATCACCCCCTAAATAGGTCAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGGAGG G[G/C]AGAAGTGAAGGAAGAAGATAGGAAGGATATTACCTCTTCTGTATTTTTTATATCTATAAATATATTAAAA GGTGGCAGCAATCTCCCTGTCCCTATCCACTGTGTAAAATTGTCAAGGTAAAATTATTGTCAAAGTTTAAAT AGCAAGTCAAACTTGGATGTATCAAGGTATCAAGGTAAAATTATTGTCAAAGTTTAAAT
WI-7919	242	T/C	GAAGGCAGGCTGGATCACTTCCCGCAGTCCTTGGGCAGCGCTTTGCTGTGGAACACGAGGAGCTCCTCCT CAGGGGCCTGGCACTCACCTTCATTCTATTCTGTATGATTGGTTAAACACTGTCAAATAAATAGAGAT GTGCCAGATTTAGATTTCTTACCCTAATCTGTTAATATTGTAACTTTATTCCATTTGAAAGTGTCA AGCCCATTCAGATAAGCTATAAATCTGGTCTTTAAGGAA[T/C]ACAACTTT
WI-7928	101	T/G	CTCCCTTCCTATGTCTCTCAGCAGCACGTTGGGGCACACGTTTCATCTTCTTGACCGTTTGCTGGGCTA TTCCCCTGCAGTGCAGACATCGTCAAAATTCA[T/G]ACAAGAGGAAAATTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTTGCACTTTAAAACTGAAAATTCAACTCTTTATATAGGATTTCTTT CTATCTCCATCTCCTCATTAAAAAATACGTACATTCGAGGTAATGGTA
WI-7936	131	T/A	TTTTGAGTCAAAGACTTAAAGGGCCCAATGAATTATATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTCTTTGGAGTTAAAATGCACATATAGACACATACACCAAACACTTACACCAAAC[T/A] ACTGAATGAAGAAGTATTTTGGTAACCAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGATGAGTATATTGTTGAA
WI-7944	99	T/C	TACACGTTCCAGCCGTTGCCCCACTCATCTGCGCGCTTGCTTTGGTTGGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCATG[T/C]AGCCCAAAGTACAGCCTGACCACCCTGGTGTG TGTAGCTAGTAAGATTACCCTGAGCTGAGCTGAGCCATTGGCATGCCAATGGACACAGTTACACTTGACAGA CAAAGATGGTGGGAGATTGGCATGCCATGGCATTGCCAATGGACACAGTTACACTTGACAGTCA

Name	Pos.			Sequence
WI-7805	101	A	G ---	TTTCTTAGGCTGTACAGTCTGATGCATGATTTTTATAAATATTTCATACTCTTGTGAATTTGGATCTT TTTACTTGAGCATATATTTTAGAATATGTGT[A/G]TGTTAAAGGATCTCCACAATGTCTGCGAGTGTG AAGGCAGGTTCATTGTGGAATAGTTAACAGTCATCTGAAAAATAAAATGAAGTAT CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAATGAAGTAT
WI-7416	137	G	T ---	GGCCAGGAGGATTAGCAACAAGGATTCATTCGTTACTTACTGCCCTTTTATCTTCCCTCTTGCCC CAGTGCCCTTCTCTCCAGCTTCATGTGAAGCTTCATGTGCAGCATACATACAGTAAGAGACTGCT [G/T]CTACTCCTCCAGGTGCAGCATACATACAGTAAGAGACTAAATCTGCAATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAAATGTCATCAG
WI-140	252	C	T ---	ATTTGAAGGATTTGGAGGGCTTTGCAGAGGAAAATAGATTCAATTGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTCAGCCAGCTCATTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTTAGTTTAAAAAATGTGTCATTTGTCTGTATTGGCATTCCT[C/ GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCCCCGGATCAAGTCGTGGCACC CATGATGGAAAACTCTTGCCATGGTTTTAGTACCCTGGACCAAGTAGTCATTCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC[C/T]GTTTAACAAAGCATAGAAATATTCTGAACAACT
WI-198	218	C	T ---	TTCATGGTCCCAAGACAGATTTTAAAGAAACAGAAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAAT GCATGAGTTTG[T/C]CCAAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCTTTATTTTGTTTTAGTTCCC
WI-205c	146	T	C ---	TTCATGGTCCCAAGACAGATTTTAAAGAAACAGAAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAAT GCATGAGTTTG[T/C]CCAAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCTTTATTTTGTTTTAGTTCCC
WI-205b	146	T	C ---	GAAGACTGAGTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGAATTCAACCTGTTGCAACCCAAGTNCTTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCCT CTCCCCCACAACACACAAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTTGCTTTAGTTTCTCAAATGGGAAATGG
WI-234	165	G	C ---	AGCTTTTGAAATCCAAAAACCCACAT[A/G]CTTGACTCTCTTATCCTCCTCCTTGTTGTTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCTGTGCCTGAACGGAGGGATGGGGCGGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTGCCCTGAAAGACCTCTCTGAAGACTCTGATGACTGGGCAAA
WI-276b	25	A	G ---	TCTGGCAAGGGCTTTGTCTTATCCCTCCTTGTCTTATCCCTGTCTTATCCCTGATGACTGGGCAAA

Clone	Pos			Sequence
WI-276	25	A	G	AGCTTTGAAATCCAAAAACCACAT[A/G]CTTGACTCTCTTATCCTCCTCCTCTTGTTGTAACATCTATCCCTGAGGCAGAAAATACAGAACACCCTGGCTGCCTGAAAGAGACCTCTCCTGAAAGACATCGGTCAATGTATCAAAGCATCTCTCTATCCTCCTTGCTATCCTGACTGGGCAAA TCTGGCAAGGGCTTTGTCTTATCCTCCTTGCTATCCTGACTGGGCAAA
WI-427	59	G	A	TTTCCCAATCCACAGGTAAAACTAATAATATGGATGTATAGAATTTAGAACTACTTCC[G/A]GTTT TTTCCCTGGGGAAAATATTCACAAAACATTGTGGTCTGCAATCAGGTTAAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCATTATTAGAGCCAGGTGCTTGTCTGTCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106	T	C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAA[T/C]AAATGGTCCTTTATTAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAAACTTCTCCACTTCC
WI-562b	106	T	C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTT[T/C]AATAAATGGTCCTTTATTAAAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAAACTTCTCCACTTCC
WI-562	103	T	C	GTGTAATTGGTGGCTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAAGATGTCTATGTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCTCCATTACCTGGTACCTCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597c	141	A	G	GTGTAATTGGTGGCTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCTCCATTACCTGGTACCTCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141	A	G	GTGTAATTGGTGGCTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCTCCATTACCTGGTACCTCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136	A	G	

ID	Pos				Sequence
WI-611	66	G	C	---	TTCAAATTTAAACACCATTGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCTCTTCTCT[G/C]ACAGTGAGACACCTGCCTTCTATTGTCCTTGACGTATTAAGCGTATTCAGTCAGCCATCTGGA ACCAAGGTTTCATTTCTGCTGGCTGTCCGCCCTCCTCACCCTACTTGGGCTCTGACTTCCTTTCCTTCCTGGGCT GAACCTTCTCTGTGTGGCGTGTCCGCCCTCCTCCTGCTTGGGCTCCAATAC
WI-681b	156	A	G	---	TGAAGCCCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTGGGACACAGATTATATGTCAGA CACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTT
WI-681	156	A	G	---	TGAAGCCCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTGGGACACAGATTATATGTCAGA CACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTT
WI-867b	119	G	A	---	AATCTTAACAGCCTTTGATGCCAAAGCCACTTCAGTCTTAATTCTTTTGGAGCCTAAGATCAGTG CAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTC[A/G]TCTCCGTTGTGTGTTGGC CAAATAATAATCTCCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGTGGTTGAATGTGTCCCCCACAAAGCACACATTAGAAACTTA
WI-867	113	A	G	---	AATCTTAACAGCCTTTGATGCCAAAGCCACTTCAGTCTTAATTCTTTTGGAGCCTAAGATCAGTG CAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGTGGTTGAATGTGTCCCCCACAAAGCACACATTAGAAACTTA
WI-867	119	G	A	---	AATCTTAACAGCCTTTGATGCCAAAGCCACTTCAGTCTTAATTCTTTTGGAGCCTAAGATCAGTG CAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTC[G/A]TTTGTGTGTTGGC CAAATAATAATCTCCCCCAGGGACGTCCTCTTCTATCCCTGAAACCTGAGAAAATGTATCTTATGC TCATCAGACCTGAGATTCAGCATGAAGTCATCACCAAAGGTACCACAAATGTAACCTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAAATGGAATGATAAGAGCACCACTACCTGTGTATGCCACTGTTGTATGGCCTGAATTGTGTACCC AGTGCTATGTGGTTGAATGTGTCCCCCACAAAGCACACATTAGNCTGTATTTGTACATAA
WI-871b	123	C	G	---	TCATCAGACCTGAGATTCAGCATGAAGTCATCACCAAAGGTACCACAAATGTAACCTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAAATGGAATGATAAGAGCACCACTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAATGCCTGAATTGTGTACCC TAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTTGTACATAA
WI-871	123	C	G	---	TCATCAGACCTGAGATTCAGCATGAAGTCATCACCAAAGGTACCACAAATGTAACCTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAAATGGAATGATAAGAGCACCACTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAATGCCTGAATTGTGTACCC TAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTTGTACATAA

ID	Pos	Alleles	Sequence
WI-884	198	T C	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGAGAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACTTTCCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAAATCCACCTCATTAATCATGACAACNNAAAAGGAATA[T/C]G ATCCCGCCATGCAACATTTATTCAGTGAAAACATGATGAAAATGAACATAAT
WI-921b	205	G A	CACTTCCCAAGGGCTCTGGGGGANGAGCGGGTGGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCGAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTCGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCACGCCTGGCCCCCAAGAAAAGTCTNGCCAGGAAAAGCACGATCCATCTAC TCT[G/A]GGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
WI-921	205	G A	CACTTCCCAAGGGCTCTGGGGGANGAGCGGGTGGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCGAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTCGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCACGCCTGGCCCCCAAGAAAAGTCTNGCCAGGAAAAGCACGATCCATCTAC TCT[G/A]GGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
WI-945c	90	G C	GGCTGGGATGAGAGGTCTACTTGTGTACTGGAGGTTCACTGGCTGTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90	G C	GGCTGGGATGAGAGGTCTACTTGTGTACTGGAGGTTCACTGGCTGTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167	C T	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTTCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C	TCCCACTGAGTATGGCTTTCAGTAGTTTTATTATGATGTGCCTAGGTACATTTGTTTTATTTGTTCTG CGAATTGTTGTATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCTTTCTGTGTTC CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCCACTA[T/C]GCTGTTTTTACTCTCCTCTG AATTTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTGTAAATNTG

ID				Sequence
WI-1147b	204	G	A	TTTGGCCATTATTTGAAGATAACCCACACCTTGGTGTCCAGGGTTTCACAGGTTATTAGTGGTCAGTCACATAGGCATATAGTACCTGTATGACTTCATTCCAGCACCGCAAACTTCTCCTGTCTGGCTCCTGAGCCAAAAACAGGCATTACCATAAATCACTTGTTAGGATGAACTTATCTGGCCAAACTGATAC[G/A]GCATGACCCACAGCCTCAGGTATATAAAAACACTCTCAGGCAGA
WI-1158b	147	C	T	GCATTCAGAGAGGGTTCGTTAATGACATTCACTGAGGCCCGTCTATGTCAGGCCCTTGGTGTTGAAGACGCAATCATGAACAAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGTGGCTAAGTGCTGGGG[C/T]TCTGGGGTCAGGCTGCCTGGGTCACATCCTGGCTCCAAACTGCTTTGCTATGGCT
WI-1158a	124	C	G	AAGTTTACAGAAAAATACCAGAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCATCATCTTCAANGTNCCCACAGACACACTTATCCCCTAGACAGCAGCCATTCTTTTGAATGN[T/C]GNCANTAAAAATGATTTGAAATTGGGAATAAAGCCCTCCCCTCTAAATGATTTGACACGTTGTTAGACCTTGCCTAGGGC
WI-1304	124	T	C	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACTCCACTNTGTCTNACAAAATNACACTGTTTTCCTCACATCCCACTGCTTTCANTAATTNACTCCACTNATGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305d	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATT[C/T]TATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCTCACATCCACTGCTTTCANTAATTNACTCCACTNATGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCCATTCTATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAGATAAGGTTTCCTCACATCCCACTGCTTTCANTAATTNACTCCACTNATGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T	C	TTCTCAATTCCAATCTGTGTGTTACTTTACTTTTATTTCTTTCCATTCTATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATAA[T/C]TNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATTGCAGGGCGGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTTAAATAA[T/C]TNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATG[C/T]AGGGGCGGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

ID	Pos				Sequence
WI-1306b	248	A	G	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNTNG GGCTGGGTGACTGTGCCTGGGTCATTTAGAAGCCATAGAAGTGAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTGTGAAGGCCAGTTGAAATTTATCTTCCTTA[A/G]GC
WI-1306	240	A	G	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNTNG GGCTGGGTGACTGTGCCTGGGTCATTTAGAAGCCATAGAAGTGAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTGTGAAGGCCAGTTGAAATTT[A/G]TCTTCCTAGC
WI-1307b	118	T	C	---	GACAAGGCTGGTACTAGTTCCAATTCCAAATCTATGTACACTTTCCTCTCCACTTTCTCAAGTGGACA GATTTTCTGCATTATACTGCTTGGGGTTGGGGGAGCAGTGGTGTAGGCCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGTGATCTATCACTGGTT TCTTTTTGGTGTTGTTGTTGCTGTTGTTTTCTCCTGTAAAGNTGTT
WI-1307	118	T	C	---	GACAAGGCTGGTACTAGTTCCAATTCCAAATCTATGTACACTTTCCTCTCCACTTTCTCAAGTGGACA GATTTTCTGCATTATACTGCTTGGGGTTGGGGGAGCAGTGGTGTAGGCCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGTGATCTATCACTGGTT TCTTTTTGGTGTTGTTGTTGCTGTTGTTTTCTCCTGTAAAGNTGTT
WI-1325b	169	T	C	---	GAGAGATGGCCAAGACAAAGCAGAGGAGAGAAGAGCAACCNTCTGTGGTTTATCGCAGCAAGCN ATGTCTGTCTCCATACCCAGAAATGAGCCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACACATTCCCACTTTACATCAGTGGGAATTGGGAACTTCCTT[C/T]CTCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTTACATCAGTGGGAATTGGGACTTGGTGAAGTTAGGTT
WI-1325	165	C	T	---	GAGAGATGGCCAAGACAAAGCAGAGGAGAGAAGAGCAACCNTCTGTGGTTTATCGCAGCAAGCN ATGTCTGTCTCCATACCCAGAAATGAGCCATGTGCTCTTGCTC[C/T]TCTTCTACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTTACATCAGTGGGAATTGGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T	C	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTGTAAA ACACCAAGTGCGGGTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGANGACTC CAGCGGACACTATGGAGCTGAGAGTCTGT[T/C]GAAGTTGGGTAGCTACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175	C	G	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTTGTAAA ACACCAAGTGCGGGTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGANGACTC CAGCGGACACTATGGAGCTGAGAGTCTGTGTGAAGTTGGGTAGC[C/G]TACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

ID	Pos	Var	Sequence
WI-1341b	136	G A	TATCAGCATGATTGTGGCTGTGTTGGACACAAAGTCAATTTGTACTTTTGNTGCNNNTCCTTTTCTNTTT ACCTGATCCACTACTCTCTCCAAGATCANGTTCAAAATTTGGCTTNCTTTGTTNAATTATACCCAAGC [G/A]GGGATTGTGATGGATCTGTTTATTTCCTGTCTGTGTTTCCCCAGCCCACTTGCACTTAGCAAGTGT GTTTCAGGATTTGTCTCTGTTTCCCCAGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192	G C	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGAGATTTCAGAAAATA
WI-1349d	264	C A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGAGATTTCAGAAAATATGAT
WI-1349c	192	G C	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGAGATTTCAGAAAATA
WI-1349b	264	C A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGA[G/C]TTCAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGAGATTTCAGAAAATATGAT
WI-1349	264	C A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGAGATTTCAGAAAATATGAT
WI-1403b	57	C T	TGGTATTTGGAATGGGGTTCAGACTCCGGGGTTCTGCCTTTGGTAAGTTGC[C/T]TCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAAATACGT AAAGTTTACATCAACATAATTCTTGCCCTGCCATCATGCATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAAGGGGTTGTATCTGATTTGT
WI-1403	58	T C	TGGTATTTGGAATGGGGTTCAGACTCCGGGGTTCTGCCTTTGGTAAGTTGC[T/C]TCCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAAATACG TAAAGTTTACATCAACATAATTCTTGCCCTGCCATCATGCATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAAGGGGTTGTATCTGATTTGT

WI-1417c	31	C	T	CAGGCCGGAAGAGAATTCACGTGGAGAGATGT[C/T]TTGGCCAGGCGGGCGGGCAGATGTGAGCCCACGGG GGTGACAGCAGCATGCCTGCTGGCCATTTGGAGGGCCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGGACTTCGGAAGTTCCGGCTTCAAAAAGCTGGGTCCGGTTTGAGGCGGGTTGC AGGCGGAGGCCCCTTAGGTCGC
WI-1417b	31	C	T	CAGGCCGGAAGAGAATTCACGTGGAGAGATGT[C/T]TTGGCCAGGCGGGCGGGCAGATGTGAGCCCACGG GGTGACAGCAGCATGCCTGCTGGCCATTTGGAGGGCCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGGACTTCGGAAGTTTAAGGGGCTGGGTCCGGTTTGAGGCGGGTTGC AGGCGGAGGCCCCTTAGGTCGCTGTATTTAATGTTTGCTTTGTGTAGAAAAGTCGC
WI-1729	172	A		CCATGAGCAAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATATCTGTATTTCTT TTTTATTCTCCAAAAGAAAATTTCATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTTGGGAGAACTGAAAAAGAGAGCTTACAGCAAAAACTCTCCACACATTCCAGCA GATGTATGTGTCCGTGGTNACCTTCTCTCCCACCATCACCTGTTTT
WI-1732b	122	T	C	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCCTT[T/C]ATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGGTGCATCAGTATATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATCATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114	C	T	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGT[C/T]AACCCTTTATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGGTGCATCAGTATATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATCATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97	A	G	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAGGTTTAAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTCACCTTGG[A/G]TTAAGGTGTGCTGTTTTCTGGCAAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCCTGACTGAG CTACATTCACTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31	A	G	GGTACACAAAGAAAATGCTTCTGGAAATCTAC[A/G]TAGGCGCCTTAACATTTGGCTGAGTATTAATC TGTACATGTGAAGTGTAATGTGAACCACCATGAAGCTGGGCAAAGAACAATTCCTAGGAAAAGTACAATTAC TGGGAAACTGTAGAACAAATAATTCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTTGAGTACAGAGAGGACATTCAAGAATAATCATCATAAAAAT
WI-1803c	77	A	G	CCACTCAGTAATAATAGTGTTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT[A/G]AGTAGGGTAGAGCAGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATTACTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCCTCAA GGAAATGGGAATACCTATAATAACAGTCTTATTGAGGAAAATAACTGGAATCA

ID	Pos.			Sequence
WI-1803b	77	A	G	CCACTCAGTAATAATAGTGTTGGGAGATAAGTATATGGTAGGCACATAATAATAATTATTTTCAGGCAGAACCATTATGAT[A/G]AGTAGGGTAGAGCATCAAAGCATGACATACTCTGGAGGACATATCCTGGGTGCTAATTTCAAATATATCTACTAAACAGTCTATTGAGGAAATAACTGGAATCAGGAAATGGGAATACCTATAAATAACAGTCTATTGAGGAAATAACTGGAATCA
WI-1837b	112	C	T	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCATTGATAATTCACTTCTTTTCCCAGGCTCAAGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]TCTGTCCCCAGTTTATTTTTAAGGTTTTTTCATTGCACCTGATGCCAAAACAAAAACCTCAAAAGACCTTGAGTGAATTTTGAGCTCGTGTAACAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1837	112	C	T	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCATTGATAATTCACTTCTTTTCCCAGGCTCAAGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]TCTGTCCCCAGTTTATTTTTAAGGTTTTTTCATTGCACCTGATGCCAAAACAAAAACCTCAAAAGACCTTGAGTGAATTTTGAGCTCGTGTAACAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1840b	79	G	T	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTTTCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTGTTAGTATATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACTATCGCA
WI-1840	79	G	T	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTTTCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTGTTAGTATATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACTATCGCA
WI-1879b	110	C	T	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTCCTTCTTTCATAACTTACTCCCCGCACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTA[C/T]GTCTGCNAAATAAACTCCCAAAAAGTGGTTAGTCCACAGGGTTTAATAGTTCTTGTTGAATTCTGTGTGCGACCCTGTGCCTTCTCAAGAAAAAAAAAACATTGAAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110	C	T	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTCCTTCTTTCATAACTTACTCCCCGCACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTA[C/T]GTCTGCNAAATAAACTCCCAAAAAGTGGTTAGTCCACAGGGTTTAATAGTTCTTGTTGAATTCTGTGTGCGACCCTGTGCCTTCTCAAGAAAAAAAAAACATTGAAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119	C	T	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNGCTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGTAAAGTGCCCTGCCCCAACGCGCACAACTAGAGAGCAGCCAACAGGTGTTGAACCCAGCTGCCTGACTTCAGATCTGTGTGCTTAACTGCCATGCCAAGAAACCACTTTTTCTTTGCTCC

ID	Pos	A1	A2	Sequence
WI-1900	119	C	T	TGTTCTCTGGTCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGC[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCCAACGCGCACAACTGAGAGAGAAACCACTTTCTTTGCTCC GACTTCAGATCTGTGTGCTTAACTGCCATGCCATGCCATG
WI-1943c	165	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGCC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGCC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1960c	270	A	T	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAAATCTAAAAATGCACCTCCCAACTTT
WI-1960b	270	A	T	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAAATCTAAAAATGCACCTCCCAACTTT
WI-1977	203	T	C	CTGATGCCAAGTGCGAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTCTTCATAGAGTNTTGTTTTAGTCTCGTAATATTACTGTTGCCCTAGGAAGGTTGTT TTTCCTACTGCGTCTGTGAAAGCCTTCCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATTT[T /C]TAACAATCAAACACTGGCTGAGGCTGTTGG
WI-2012	102	T	C	AAATTCTAGAAGCCAGAAGTCAGCTCACGATTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAAAACTAGCTAAAAATC[T/C]TTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCGTGAGTCACTTTTTCTACTCTCATT GGCTTCACCAATGCTTCCACTGGATC

ID	Pos	Allele 1	Allele 2	Sequence
WI-2013	127	C	T	CTTTAGAGGTGGTCATTTCGGTTCCCTTCTGGAAAGTGATTCGTGTTTAAGAAAAATAGATGCAACG TTGCTAAGTACAACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACT[C/T]CTCA CCAGAAAAAGAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGGATATCTCAGCTTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166	G	A	ACCAGACATCCCATCAGGAGGTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTTCTAGATGTACAC[G/A]TGTGGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTGGTTAGGCTCACCTTCCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032b	219	C	G	ACCAGACATCCCATCAGGAGGTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[C/G]CTTCCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032	219	C	G	ACCAGACATCCCATCAGGAGGTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTTCTAGATGTACAC[C/G]TGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[C/G]CTTCCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2054b	188	C	T	CGTTTTCTTCTACATCTTGGGGNACATAAAGANGAAAGAAGNAGCTGTCTTTTTGTGGTAGTTTTGCT CAGAGCTGCCTAGAGCNAGGACNAGGACAAGACAGGTGACCTTCAAAATACCTTACAGAGATTGGA TTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATAACCTGCT[C/T]TCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGTCTT
WI-2054	183	T	C	CGTTTTCTTCTACATCTTGGGGNACATAAAGANGAAAGAAGNAGCTGTCTTTTTGTGGTAGTTTTGCT CAGAGCTGCCTAGAGCNAGGACNAGGACAAGACAGGTGACCTTCAAAATACCTTACAGAGATTGGA TTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATAACCTGCT[T/C]TCCTCGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGTCTT
WI-2573d	129	T	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTCTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCTAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTTGGGCTTGGACGAG
WI-2573c	165	A	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTCTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCTAGGGGTAAGCAAACAGAGGCTGTGT TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTTGGGCTTGGACGAG

WI-2573d	129	T	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACATTAACAGCAGTAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTCCGTGCTT[T/C]TGATATCATCTGATCTTCCCAACCAGGGCTTATTTATGCCTAGGTAAGCAAACAGAGGCTGTGTGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTTGGGCTTGGACGAG
WI-2573c	165	A	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACATTAACAGCAGTAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTTTGATATCATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGTGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTTGGGCTTGGACGAG
WI-2573b	165	A	C	TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACATTAACAGCAGTAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTT[T/C]TGATATCATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTAAGCAAACAGAGGCTGTGTGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTTGGGCTTGGACGAG
WI-2573a	129	T	C	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAAGAACAAGCTTTCC[A/G]CTCCCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCCACTTAAAGAGAGGTTTCTTAGGTCCTCTGCATATCATGGAAGCCAACTACTCTATTAACGCTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTACAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAAATATCGATATAC
WI-2868b	60	A	G	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAAGAACAAGCTTTCC[A/G]CTCCCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCCACTTAAAGAGAGGTTTCTTAGGTCCTCTGCATATCATGGAAGCCAACTACTCTATTAACGCTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTACAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAAATATCGATATAC
WI-2868	60	A	G	CATGCTGTGTAACCTCTGTGCTGCTTGCTGTCGGGGAAATTAGAGCAAGGAAATTGTATAATCCTAGGCTTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C]AGAAATGAATAGAGCCCATTTAAATTATATCACAGCTTTATGTCCCACTTCCTGTTCCTGCCATCACTGGGCTTTTTACAAAGGAGGGCTTT
WI-2870b	131	T	C	CATGCTGTGTAACCTCTGTGCTGCTTGCTGTCGGGGAAATTAGAGCAAGGAAATTGTATAATCCTAGGCTTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C]AGAAATGAATAGAGCCCATTTAAATTATATCACAGCTTTATGTCCCACTTCCTGTTCCTGCCATCACTGGGCTTTTTACAAAGGAGGGCTTT
WI-2870	131	T	C	CATGCTGTGTAACCTCTGTGCTGCTTGCTGTCGGGGAAATTAGAGCAAGGAAATTGTATAATCCTAGGCTTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C]AGAAATGAATAGAGCCCATTTAAATTATATCACAGCTTTATGTCCCACTTCCTGTTCCTGCCATCACTGGGCTTTTTACAAAGGAGGGCTTT

WI-2954c	49	T	A	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGCATAAAAAAA[T/A]CAGCACCTGGGGCACAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2954b	41	A	G	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGC[A/G]TAAAAAAATCAGCACCTGGGGCACAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2954a	38	G	T	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAA[G/T]GCATAAAAAAATCAGCACCTGGGGCACAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2971b	62	T	C	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]GCTGCCAGCACCAATAAGCTTTCTTCAAAACAATTGTGTAACCTCCTCCTTAATAAACCTAACATTTCCCTTGTTCCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTATGTCCCAGATTGCAATCCTAGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT
WI-2971	62	T	C	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]GCTGCCAGCACCAATAAGCTTTCTTCAAAACAATTGTGTAACCTCCTCCTTAATAAACCTAACATTTCCCTTGTTCCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTATGTCCCAGATTGCAATCCTAGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT
WI-2995d	133	A	T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTT[A/T]AAATCTTTCTTTCTGGTTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G	C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNAATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A	T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTT[A/T]AAATCTTTCTTTCTGGTGTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT

Clone	Pos	Allele	Sequence
WI-2995c	151	G C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNAAATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCAAAAGGAAGGAGCTGGANTTTTTT[A/T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995e	151	G C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNAAATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNAAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTT[A/T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85	C T	GTGGTGCAGTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCACATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCCTTACTCCTATCCTGAGACTTCTTCCTGAATGAATTACATGCACTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACTTGACCTAAGACAGAAATCTTAGTAGCCAAATACTTTGCAAGG
WI-3234b	68	T C	ATTCTGTAATGTTTTCACTGCTTCCAGTAAAATTCTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGAACAACAACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTGTATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATTACATCCTTATAAGCATATCAAAATTTTACTCAGTAATTCAGAGAAGGACAATGGAATGTACTTATTTNATATCTTAT
WI-3234	68	T C	ATTCTGTAATGTTTTCACTGCTTCCAGTAAAATTCTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGAACAACAACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTGTATATTTTAAACAAGTACTGTAGAGTNATGAATGTACTTATTTNATATCTTAT

WI-3292b	106	G	A	GTTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCCGTCCCAAGCCTATGGTACTGGCT[G/A]TGGTATTGGATTGGATGGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTAAGTAAAAATATTATTTNCCATGA GACACAATGGAAAAACATTCATGGAAAAAACCCATTTCAATC
WI-3292	106	G	A	GTTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCCGTCCCAAGCCTATGGTACTGGCT[G/A]TGGTATTGGATTGGATGGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTAAGTAAAAATATTATTTNCCATGA GACACAATGGAAAAACATTCATGGAAAAAACCCATTTCAATC
WI-3355	19	G	C	CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCCTCCTTACTGGAGAGGGATCCA CTTTTAAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTTCCAAGCACTTAAACTCATCAGAA AAAAAAATCATCAAAGTCGAAGTTAGTTTTNATTACCTTCCACCTTTCAATGGAAAACTTTATAA ACTGTGGGATCAATTTATATTACTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G	A	CCATGAAGAATGAGTTCCTCCTCCCCTGGGTCACGTCTAAGAATAGCACACCCTTGAGAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTCTAAGACACCACCTTATGCTTTCNAAGCTTT CTGGAATTGGGATGAATCTNACATTCAATGTGCACCCTTCGTGTGGGATCACTTCTCC[G/A]TGCCCC ATCTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAATCAGG
WI-3505b	131	G	A	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTTAAAAATTATTT GAAAAATTGCCATTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTTGCATAT
WI-3505	131	G	A	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTTAAAAATTATTT GAAAAATTGCCATTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTTGCATAT
WI-3564b	177	C	T	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGGAGTCACTAAATGTTTGAGAAATAAAAGT GAAAATCAATGTGTCTTCCCAGTGTATTCACATGGCACAGTGTCACAGAGGGCCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTT[C/T]AACAAGTGTTTGTTGGTGTCATC AGTGTCACACATGCTACCTTCCTTCACAAAACAAA
WI-3564	177	C	T	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGGAGTCACTAAATGTTTGAGAAATAAAAGT GAAAATCAATGTGTCTTCCCAGTGTATTCACATGGCACAGTGTCACAGAGGGCCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTT[C/T]AACAAGTGTTTGTTGGTGTCATC AGTGTCACACATGCTACCTTCCTTCACAAAACAAA

ID	Pos			Sequence
WI-3649	64	A	G	AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTCCTAGTATTCCTTTAGTGGAAGATTCAC[A/G]AGACCAGTTGCCTTCACTTAGTAGGGCCAATGATAGACTTTTAGGTGCTACCACAAGGGTACCTGCACAGCCACATCATATGTCACAGTATGGTTGCAAAGGACCTGTCTGCAAACCTCAGAGCCTTTATTCCTGTTTACCATATTAAATGATGACAGTAGCAAGCTCTTCTGCCTGCCTGGTC
WI-3674b	133	G	C	ACAGTACACATGGCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTATAGTAATTAAAATATGTTTATTAGAAAATAACAAAAT[G/C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTAAAATTGTAACTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTATGTTTNATTACTGCCAATCACAGCCAAG
WI-3674	133	G	C	ACAGTACACATGGCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTATAGTAATTAAAATATGTTTATTAGAAAATAACAAAAT[G/C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTAAAATTGTAACTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTATGTTTNATTACTGCCAATCACAGCCAAG
WI-3682	137	G	A	CAATATAGACCAAATGACTGCCACAAAGAGAAATTAGTGGATCTACATTAGAAACCACATGTTTTATTGGCTCTCTTCTCTCTCTTTAATGCTCTCCAACACCAATTCACTTATTCTTTCAATT[G/A]AGCATTTGTCCAATTAAAGTCAATGAAAAAATAATGTACATTTTCAACAAGTATACATTAAGCCCTGCAAAAGTGCTTATATGCTAT
WI-3854b	194	G	A	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGAGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTCTGGTTCAGGAAGGCAAGGGCAGTTATGCACCACTTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAAGTTAAAATGGCCTGTCCCACTCCACAGAAATGGTATAACAGAGTCAGAGCCA
WI-3854	194	G	A	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGAGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTCTGGTTCAGGAAGGCAAGGGCAGTTATGCACCACTTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAAGTTAAAATGGCCTGTCCCACTCCACAGAAATGGTATAACAGAGTCAGAGCCA
WI-4039	210	G	A	AGCCAGCCACCACATCATGTTGAGTCCTGCTCATTCTTCCATCTCTTATTTCTCTCTACTGCCTTCACCTTCCATTAACAGAGAACTCTTGTGATTACATTGTGTTGGTTACACTACAGAATCCAAGATGACCTCCCCATCTCAAGGTCAACTAATTAACACCTTAATTCTATTGCAATCTTTGTCATTACCATAACATATTCATGG[G/A]TTCTGGGGATAAGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130	T	C	GAAAAATGATGTTTTTGATTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGTAACCTTTTATTTGATGAAAACTCTGTCTATAATTAAACCTTCCTCTCTCTTATTTGCC[T/C]ACAGTTTAGGTAAATAAAAGATGCCCAAGAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGGGTAGGGACAAGTNCAGAAAAAGGGAGGAGGAGGGTTTTCTGGGAAGA

				Sequence
WI-4110	130	T	C	GAAAAATGATGTTTTTGATTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAAACTGATAGT AACCTTTATTTGATGAAACTGTCTATAATTAAACCTTCCTCCTGCTTATTTGCC[T/C]ACA GTTTAGGTAAATAAAAGATGCCCAAGAATTCAGTATTCAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAGGGAGGAGGTNGGGGGGGTTTCTGGGAAGA
WI-4119b	168	G	A	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAAGAACAGAGAAGGAGGGGTT AGAGGAAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTCTTTGTTTTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168	G	A	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAAGAACAGAGAAGGAGGGGTT AGAGGAAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTTTTTAAAGGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51	T	G	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAATAGAAAAGTG[T/G]TTTAAACTATTT CAAATAAACAATAAAGAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAATTAGTGGGG TTCTTCCATGACATTGGCTTGTTCTTCTCTCAACAGTGGGTGGTTTTGGATGTTTCCTATGCTTTCTC AGGCACACAAACAACAGTGAAGAACCTTTAGCAACATTCTGAATGTGTG
WI-4123	51	T	G	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAAATAGAAAAGTG[T/G]TTTAAACTATTT CAAATAAACAATAAAGAAAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAATTAGTGGGG TTCTTCCATGACATTGGCTTGTTCTTCTCTCAACAGTGGGTGGTTTGGATGTTTCCTATGCTTTCTC AGGCACACAAACAACAGTGAAGAAACCTTTAGCAACATTCTGAATGTGTG
WI-4149b	145	G	C	TTGTACATGTTCATTCATCCCTCCCCCATTCTTTTCTGTCTTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATAC[GTGCTGT[G/C]CCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCCATGATATAAGGTAATTG
WI-4149a	137	T	C	TTGTACATGTTCATTCATCCCTCCCCCATTCTTTTCTGTCTTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATAC[T/C]GTGCTGTGCCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCCATGATATAAGGTAATTG
WI-4182	188	G	A	TAACACACTTTTCATTTGGTTCCTATTACTGCAGTTAAAGGACCATCCATTATATTACAATTCCCTC AGTTCTATGCTTTAGAGTNCTATTATAGGACTACTGTAAAATTTCAGAGGGAATTACTCCTTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAAATTGCAGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCTTCCAAGTTCTTAAATTCCTAG

WI-4230	93	T	--	AGAGACGTTGAATGGGGACATCTTTCTATTCGATTTAGTTAACATTTGATAAGAGAATTGATGAAAGTTGTCACATTCCAGATTTATCTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACTTTCCATGGTAAAAAGGAGGAGAATGAATAGTGACCTTTGAAATTTGAATACATTTAAATGGAGGAGAATGAATAGTGACCTTTGAAATTTGAATTTATGG
WI-4241	118	C T	---	GAAAATTCCATTGAAGTTTGACCTTGAACTGATCTCATTAATACTTTTNCTTGTAGTGGTTGTATTTCATTTTGACAACAGACAGACGAAAATTTCCACTTAAAATTAAATTCTC[C/T]AAGTATCTATGATTTAGCACTGTTAGCACCAGAAACTGTGAAATTATCTCCTAGATATTCTTCAGAATCTAGGATGGAAGAA
WI-4271b	151	A	---	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGAACTGGACCTAAAAGACTAAGCACATTTCAGCATCAACAAAAGGTGACACGTTACCCATGAAAGGTCCCTGGAGGATTAAAGATCAAATAAAGAGCCTCAGGGGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGCCCCAACCCTCCCCCCTTTGTCTCAGGCTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151	A	---	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGAANCTGGACCTAAAAGACTAAGCACATTTCAGCATCAACAAAAGGTGACATGTTACCCATGAAAGGTCCCTGGAGGATTAAAGATCAAATAAAGAGCCTCAGGGGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGCCCCAACCCTCCCCCCTTTGTCTCAGGCTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156	G A	---	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTTGTGCCCAGTTTAGCATATGAAATTTGAAAGGGATGAACCTGGAGGAAGAAGAATAGAAAAGGATATTATTGCATAACCTTTGGAAGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTAAGAGGTATTGTGTAGGAACTGGAAGCGGTAA
WI-4389	156	G A	---	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTTATGATATTTGTGCCCAGTTTAGCATATGAAATTTGAAAGGGGATGAACCTGGAGGAAGAGAGAATAGAAAAGGATATTATTGCATAACCTTTGGAAGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTAAGAGGTATTGTGTAGGAACTGGAAGCGGTAA
WI-4488	31	A G	---	GATGACAATTATTGTGTATTGGCATTTAAA[A/G]GTACCATTCCATTTCTTCTCTGGCTTTCGTGTGTTTGTTGTTGGAGAAGTCAGGGGTTAGTCGTATTGCTCCTTTCTAGTTCTTCTCTCAGTAGGAAGACTGATCCTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTAAAGAACATAAATCAAATTGTATTATCCTATGCTTAAAAATGCTCAG
WI-4491	145	G C	---	ACCATCAATGTATCACCTTCTAAAATTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAAACCTGTCTTGGACATTGAAAATAAAACATTACTATTGGTCATTTCTGCTACTTACAAAGGTACTGCACTAAACAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAATTTCTACCACTGTCATTTCTTGTCCCCATAAATAAAAATTTTACATGCCT

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WI-4584	144	A	G	TTGGTTGGCATTTAGCCTCCATAACAACTATTACAATCATAATTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGCAGAGCCAAGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAAAATGTTAATTAAAAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAATAGGTGTGCTTTAATTGTTTATCAGTATGC
WI-4639	185	C	T	TTTCTGCATTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATATCAGAGAGATCTCAGTTAACTTCCAATTCCACCATTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTGTA AATTTTAAGGACACCTATCATCGTAATATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A	--	AAATGAATCCGCTTTAGAGCAAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGA[A/--]GATTACTCATAAAAAGCATATTAATTTTATAAATATGGAAAATTTAACTAGATAATTAAAATGTGAAT TGAGTTTGAAGGTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCGGATGACAATGATGAACTGTTCTAAGCAGACAG
WI-5390	87	A	--	GCTTTTGAGAATGAAAAGGGGAGCCTGGACCATTGCCAGGCCTTCTTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTTAT[C/T]GTCTGTCTCCCCTTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCCAGTCGCCTGGCCCGATTCGTGGCCTCCTAGAGGGTGTCCAGAAAAAAAGTTCGGTGAATAGAATTG ACGAATGGGTTCAGAATTCGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G	A	CCTTGCCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAAACATTATTTAATTT[G/A]AAAAGAAAACTTGTTCTGAAACTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCATCTCTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTCATAACAA
WI-5404	87	G	A	CCTTGCCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAAACATTATTTAATTT[G/A]AAAAGAAAACTTGTTCTGAAACTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCATCTCTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTCATAACAA
WI-5545b	77	A	C	TAGGAAAGGGGGATGGTGATGGCCTCTGAGACATTAAATCTATTCTTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTGGCTGACTTGGCTGAATTTGCTACAACTCCAAAAGANTC GAGATACACCATGAATTTTATTTTCATTTCA
WI-5545	77	A	C	TAGGAAAGGGGGATGGTGATGGCCTCTGAGACATTAAATCTATTCTTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTGGCTGACTTGGCTGAATTTGCTACAACTCCAAAAGANTC GAGATACACCATGAATTTTATTTTCATTTCA

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WI-5860b	134	A	G	ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTGCTAAGATTTTATTGT TTCTTTTTATATAAATTATGGATTTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/ G]TTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A	G	ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTGCTAAGATTTTATTGT TTCTTTTTATATAAATTATGGATTTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/ G]TTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C	G	GCAAACAACCTATTATACCTGATTCCAACCCAGGTCTACTAACATTAATCAACCCTAACCACAATAC TATATATTGTCCGTTCTGAATTATTTCATTTAGAATCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGCTTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG TAATT[C/G]ATAGTAGGTCACCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAACC[T/C] AAACCCTATATTNCTGTCTGTGCATACTTTAAAATGTATAAATGTGGGAGAGAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109c	147	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAACCTAA ACCCTATATTNCTGT[T/C]C]TGTGCATACTTTAAAATGTATAAATGTGGGAGAGAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109b	147	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAACCTAA ACCCTATATTNCTGT[T/C]CTGTGCATACTTTAAAATGTATAAATGTGGGAGAGAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109a	129	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAGAGAAGGAATTTTGATGT AAACCCTATATTNCTGTGTGCATACTTTAAAATGTATAAATGTGGGAGAGAAGGAATTTTGATG GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6112	96	T	C	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGA[T/C]GCATATCCCAAGTGCCTTAGCACATGCCTCCCATAC AGTGAACAGTATTTGACTAAAACATACTTGTTAAATCAATAAATTAATCAACTTGGCATATGCAGG GAAC

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WI-6244	103	T C	TAATTGCACAACTTACATATCAGGGTTCTGATTGAAAGGAAGAGAGAATATTCCTTTCTTTTAGTGATTGCTTAATATTCATAAGAATAAGTGCACCATCTCT[T/C]GCTCCTTATAAATGTGTTAGAAGAAGGAAATTGAGTGTTGGGAATTAAGCAACCAGGAGACATTTTATATACTCCTACAGTGGGGGAAGACTTCCTATTTCTTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	C T	CTGGCCTTATAATCCAAGTTTAGGATTAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTTGTCTACAAGATTTCCTCCTAGTAGGGCTTTGGGTGTTGGCACCGTTGGCTCATTC[C/T]ACTCTCCCTGGGTCTTATTGACTTCAGGGAGGCCTAGAAGAGAGTCG...GGGTTCCAAAGATTTCGTTACGATTTTTTA
WI-6336b	234	C T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCCATATATTCCCCCTTTACAGTGTTTTCTTATAAGACATACAGTTAATCAATTAACAAACTAAACAGCTTATATACTGGCAATATATTACAGATGGGTTTATGTCAGACTAATAGATCACACTGAAATGGACCATGTGGTACCCCAGTCGCATTATGTCTTGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6336	234	C T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCCATATATTCCCCCTTTACAGTGTTTTCTTATAAGACATACAGTTAATCAATTAACAAACTAAACAGCTTATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACACTGAAATGGACCATGTGGTACCCCAGTCGCATTATGTCTTGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6381	92	C A	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTACAAAAATGGNTTCATGTTTAACAA[C/A]GTATTTTAAAAACAGGCACAATATTCTAANGGCATATGCATTCCACCATGGCTTTGAATGTCCTCCCAACTTCACAATCAAAATCTACAGANGCGGCAAAAGATCAGAGTTCAG
WI-6436	198	C G	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGTTCAGAGGCAAAGTCATGACAGAACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAAATTTTGGTATCATAATAAGAAGTTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGGTAGCGGTT[C/G]ATTGGGTGTATTCCACAGCAAGGTGATGTTCTAAGATTGATATTTATTGT
WI-6449	186	C T	GAGGCCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAAGGGTTGATATCTAGCCTATATGCCATATGTGTATGGCTAGTGTTGTTCTGATTGGTTGGTGCTCACACTGCCCCAGATTGTTAAATATTTTGAAAATCGTATCTGGTTCTATTCATCTGCATTCTCTATGTCTGCGTCTATT[C/T]ATCCCTATTCTCTGATCTTATGTGCTGAAGTTCCTCTCAATTTTTCTGTGGTGTATTTATA
WI-6449	186	C T	GAGGCCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAAGGGTTGATATCTAGCCTATATGCCATATGTGTATGGCTAGTGTTGTTCTGATTGGTTGGTGCTCACACTGCCCCAGATTGTTAAATATTTTGAAAATCGTATCTGGTTCTATTCATCTGCATTCTCTATGTCTGCGTCTATT[C/T]ATCCCTATTCTCTGATCTTTATGTGTCTGAAGTTCCTCTCAATTTTTCTGTGGTGTATTTATA

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WI-6463	72	T C	GCTGGAGAGAGAAAAGACCTCCAAAAGAAGAAGAAACTAAATCAGAGTCTCTTGAGCAAGAGAGGAATTGAAA AGAACA[T/C]TGAAAAAAATTAAAGTAGAACTCAAAGAGCCAAAAAGTCCCAATTGTTCCATTA TAAGAAATATTTTGAATGGAAATCTTAAGATAGATTTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATATGACATTCCGCATGCTG
WI-6474b	76	C T	AAGCAGTAAATCTTCCATCATGCCATGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAAGGCACAGAGAAAAAGGGGTGTACTAGAGGAACTATGTAAGCAG AGGTATAGAGAGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76	C T	AAGCAGTAAATCTTCCATCATGCCATGGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAAGGCACAGAGAAAAAGGGGTGTACTAGAGGAACTATGTAAGCAG AGGTATAGAGAGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175	T A	GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCCTTCGAGGCCTGTCTATATGCTTTATTTTTGTGA CACTGTCTATTTACCCTCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCCTCCTCGTGAGGACCTAGACACAACTG
WI-6478	175	T A	GAACTCAATTAACTTTGCAACACTGAGAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCCTTCGAGGCCTGTCTATATGCTTTATTTTTGTGA CACTGTCTATTTACCCTCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCCTCCTCGTGAGGACCTAGACACAACTG
WI-6559	149	G A	CACATTTGAATGCAACTGAGAAANTGGTTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAAACATGCAAAACATAAGGCAACAATTCTGATCATTTATAGGNTCCCAGCCCA TTAGGCAATATCTTA[G/A]TCAAATTTAAAAAGAACAGGAAATAAGGAAGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54	G A	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTGTCCTGAAAAATCTCAATTAATTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATTGAAGGCATTTGATTAINATTTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGGAACATGCATATGACTTTAAAATAAAGACCAACA
WI-6564	54	G A	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTGTCCTGAAAAATCTCAATTAATTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATTGAAGGCATTTGATTAINATTTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGGAACATGCATATGACTTTAAAATAAAGACCAACA

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WI-6608b	46	C	-	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGCCTCAGT[C/-]AGTTCAGGCAGCTAAAGGGAGGGGGGATTCCTCCTAGTCCTCTCCCTAGAGCTAAATATGCATCTGGGAAAAATTAGGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTGAACTCCCAGCACTAGGTAAAACTGCAAAAAGAAAAAACACCTGTGCCCAGGCCACTAGCTACAAGGCCACCAGAAAAAGGAA AGC
WI-6608	46	C	-	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGCCTCAGT[C/-]AGTTCAGGCAGCTAAAGGGAGGGGGGATTCCTCCTAGTCCTCTCCCTAGAGCTAAATATGCATCTGGGAAAAATTAGGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTGAACTCCCAGCACTAGGTAAAACTGCAAAAAGAAAAAACACCTGTGCCCAGGCCACTAGCTACAAGGCCACCAGAAAAAGGAA AGC
WI-6666	68	C	A	GTTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACTTTTCCAAAAACGAGGAAAACCTCCCCA[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCGTGCTTACTCTGTTGGTTTCATGTAAATGTTTGGGGTGACTCATTCCGCCTCTCTNTTCTCAAGTTCCAGGCTTCTTGGGTAGACCAAAACTAATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120	A	G	AGATTAACACATAATTATACTGGGGCCATTGTAGGGTTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAACAGAAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCAGCATTGCCATTCAGGGCCGGAGTCAGGGTTGTGGGCCGAGAAGTTTAGACAATTGGGGAATTCTGAAAAAAAAAGAAATACAGAATTGTAACACAGACACAGAATCTTAGAAGGGAT
WI-6670	120	A	G	AGATTAACACATAATTATACTGGGGCCATTGTAGGGTTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAACAGAAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCAGCATTGCCATTCAGGGCCGGAGTCAGGGTTGTGGGCCGAGAAGTTTAGACAATTGGGGAATTCTGAAAAAAAAAGAAATACAGAATTGTAACACAGACACAGAATCTTAGAAGGGAT
WI-6704c	33	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGAACATACATAAAATCAAAATCATACCATATAAACGTTACAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCCACATGGTTATTTCAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGAACATACATAAAATCAAAATCATACCATATAAACGTTACAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCCACATGGTTATTTCAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGTTTAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCCACATGGTTATTTCAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106	G	A	---	CCATGGACAGTTAATTAGGAGAAGCTTCGACTTGTTAGAATAACAGAGAGGAAGTCCCAGTTATCTACCTATTCCTTAAAACACATTTTGTCAGGCTGGAATGATTCCC[G/A]TAGTAGAACTCAACATCCACACCTGCATAAACATCGCCCTCCCAAGTGACTATTTATTACTGAGTCGACACAGGATGTCACCAGTGAGCCTCATCTCCAGTCCAATGGAGAGGTTGACTTGACCTTCCTTGGACACAGGAGGGTC
WI-6766b	148	G	C	---	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAACATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGTGCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTCTAGGGNTCTGCACACATATTTATCACTGAGAATTTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6766	148	G	C	---	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAACATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGTGCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTCTAGGGNTCTGCACACATATTTATCACTGAGAATTTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCTTCTTC
WI-6787b	97	A	G	---	ACAGATAAAAGTCTTTATTCCCCTGTATGTTACATAAGAAAGTTCTTTACAGACTTTTTTTTATACAATACTTGTGCAGCAATGTTCAAATTCAC[A/G]TTTTTACTGCATAAGATATCTTCATGTGTACAACTGTATGCTTTGTTCTTGTGGGAAGGACGCGTTAAAGACCTATGATAAACACACACCACATGACAAAGGAGAGTGCAATAGGGCAGAGAGTAGANTACTCACGGAAAAGAGTAAATTCAGGT
WI-6793	105	C	G	---	GAACCCACCAGGTCCTGTATTTATTAAGGAGCATTACATTATGATAGCAAGTTCAACACATTCATCAACAAGGCGGTCTTCAAATCAATCAGTCAACCCCC[C/G]GAGTTAGAAAGTAGAGTCATGAGGAATCAACAAGGCGGTCTTGGCTGTAGGAAGTAGGGTTAATGCCCCTAATCCCGGAAGGGGCAGACTGAAGCCAGAGCCAGANTCCTGGCAATTCACCAGTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37	T	C	---	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACAAAGCTCAAACGNACCTACAATAAGTCTAGTTACGNGCCAAGGGATAAGGCTGAACAATAAATTAACCCTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACCACTAAGNAATATTTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T	C	---	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACAAAGCTCAAACGNACCTACAATAAGTCTAGTTGTTACGNGCCAAGGGATAAGGCTGAACAATAAATTAACCCTTAAAAATGTCTATGNACAAGTACAATTTTCTTTTGAGTTCTGCAGAGCAATGACCACTAAGNAATATTTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C	A	---	GCATGATTAAACCAGTGCAGAAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTTGTAATCCAGTTAAGACCATCAGCATATACAACTCAACATCACTACTAACTCAACAATGTAGCTGCAGGGTAAC[C/A]TGTGGGATACCCTGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG

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WI-6817	145	C	A	GCATGATTAAAACCAGTGCAGAAAAATACCAAGTACACATTGGGTGAACGATGAGCTAGCTGTTGTTCTAGTATTTGCTTTTGTAATCCAGTTAAGACCATCAGCATATACAACATCACTAACTCACTAACAATGTAGCTGCAGGGTAAC[C/A]TGTGGAATACCCTGTCTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCAAAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG
WI-6819b	221	C		GATGGAAAGCCATTTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCACCCTGAATGCCAGCAATACCTGACTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGTACACATTTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTGCTTTAGCAAACAGCAATAACTTTGTGTTCCTATATGACACCTAATATCCAG
WI-6819a	175	G	T	GATGGAAAGCCATTTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCACCCTGAATGCCAGCAATACCTGACTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGTACACATTTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATTTTGCTTTAGCAAACAGCAATAACTTTGTGTTCCTATATGACACCTAATAT
WI-6826b	154	A	G	GCAAAAAGCTTTATTGGCTCCAACAAAATTATCCCTTTAAAACTCCTCTTCTTCTCTGGTCTCAGTGGAACAACACACATTTGAATTTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAATACATGCAAAAACCTTGTACAT[A/G]GAGCTAAATAATATCAAAATGCAAATATAGATTGGGTGCACTGTTAAGCTGAATTGCAAATTATGGCAACACACTGGACTGGGTATACGTTG
WI-6826	154	A	G	GCAAAAAGCTTTATTGGCTCCAACAAAATTATCCCTTTAAAACTCCTCTTCTTCTCTGGTCTCAGTGGAACAACACACATTTGAATTTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAATACATGCAAAAACCTTGTACAT[A/G]GAGCTAAATAATATCAAAATGCAAATATAGATTGGGTGCACTGTTAAGCTGAATTGCAAATTATGGCAACACACTGGACTGGGTATACGTTG
WI-6857a	122	T	C	AGTGCAAAACTATTTTGAAACAAAAGTAAACTAATGAGTCACAGCATTCAGCAGGAAGACATCAGACACGGAAGAGTGAACAATATTCACTAAGTAAAATACAGCAGATGAGATGTCTCTCACATGTA[T/C]ATTTAATTATTCATGCTTTTTCAATAGTCTCTTAGTCAACTTCAGTGCAAACTTTGGCAACTGTTTGGGCTAATTAACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153	G	A	TTATAGAATACTTATGGGGCATAACGNGTAAATGAACTGTCAACCTTAAAATCTAAACAAACAGCTTGTTTGTGGTTCGTCGTCCTGAAATCCTCCCCTGCTCACAAAACCAGCTACTINGGTTTTCTAAAAGACGTAATTTTGCAGGCAAACTTC[G/A]TAGAGGCCAAACTTCTTGCGCGTGTTAGAAACTGAGCTCATTAA
WI-6909	73	C	T	ATTGAAAAACTGGTTAGCAACAAGACAGATAAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGAAGAATGCAGACTTA[C/T]AAGCTTATAGAGAAGAAAGTCAAAAAGGAGCAAGTTTTGAAATCAGATTTTATGATACGGAAAAAAATTTCCTTTTTGCCAACAGGATTATTCGCCAACAGGATTATTTGGCAACATTTTTATACGACAAACACCATTTCCACAATATTTGCATGCCCCCTAGTTGCCTATTTTATACATATC

ID	Pos	Allele	Sequence
WI-6910b	163	G T	CACTCAAAACCTTTATTCATTGATTTACAAAACTGTACAAATATTTACAAAGTTTAGGCATTAATCCCATATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCATGGCTCTCTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAATTAATGTGGTAGAAAAGTCAGAGTGGCTGACCAGTCCCGGACCTTCCATGTGAATGACTCTTCCTGGC
WI-6915	144	A --	GCTTGTTTTTTGTTTTTGTTTTTAAGTGACCACCTTGGCCTTGTGGGCATTCTTCACTTATCTTACCCAAAAGTGCCTTGGGCCCAGCCACTGACTGATTTAAAAACCCAGAAATGTGGTTTTAAACAATGTGGTCGTGGTGAATTCAGGTGATTTNATTTCTATTGGTAGTATTTTCAGATTTCCCACAAGAACATGTATTGTCTTGTAATTTGAAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T C	CAATCAAAAAGTTCCAAGTTCAAAGCTGGGGATGAAAAGCCAGGTCTTCTGCACTTGCACTCTGTCACACTGGATTTTNCCTCTGATCCAGCTGCAGCCTCCCATAAGAAGTTCACTCTTAATTCATGTCCCATGCTTTGTCTTGGTCCCTGTGAGGAAAAGGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGGTAGGTATCCTGGCAAGATATTTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C	CAATCAAAAAGTTCCAAGTTCAAAGCTGGGGATGAAAAGCCAGGTCTTCTGCACTTGCACTCTTAATTCATGTCCCATGCTTTGTCTTGGTCCCTGTGAGGAAAAGGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGGTAGGTATCCTGGCAAGATATTTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGACTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCCAATCCTAGGTAAGATATCAAGTTACAAANTACAAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAATAAGGCTTTAACCAAAGC
WI-6955	79	G A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGACTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCCAATCCTAGGTAAGATATCAAGTTACAAANTACAAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAATAAGGCTTTAACCAAAGC
WI-6957	47	C G	AAAACTAAAAACCCTTATTGTCTCCAAGTGTGTGGCAAAATAGAAAAT[C/G]TTTCAATTACATTAGGAAATCGGGTGGATAAGGGAGTAGTTATTCCACTTAAGAAGCATTCCAGTCAAATAATCACAAAAACAAATTCAGATTGCTTGGATCTTATGGCTTGAAGAACTGGATTTGAAAACCACTTTAGGCTAAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242	G T	ACTTCTAGTGCCTCTGTTACCACCACTCTAATGCCTCTGGTCGCCGCCACTTCTGATGTCCGTAGGCCTTAAATCTGCCTGGGCTGCCCCTCCCCTGTCTTCAGCACCCAGAGGCTGGGAGAGCCGGCAGTTCCCTGCAGGAGAGAGGGCGCTGCTGGACCCCTGTCCTGACTCTCTCCTGATGGTGGGCCCTCGTGCTCTTCCTTCCG[G/T]GTCGGATC

ID	Pos	A1	A2		Sequence
WI-6996b	242	G	T	::	ACTTCTAGTGCCTCTGTTACCACCACCTCTAATGCCTCTGGTCGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCCTCCCTGTCTTGGACCACCAGGCTCAGTCCCTGTCTCTCTGCCTCTGACT CAGGAGAGGAGGGGGTGCTGGACCCCTGTGCTCTTCTCCG[G/T]GTCGGATC CTCTCCTGATGGTGGCCCCTGTGCTCTTCTCCG[G/T]GTCGGATC
WI-6996	228	T	G	::	ACTTCTAGTGCCTCTGTTACCACCACCTCTAATGCCTCTGGTCGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCCTCCCTGTCTTGGACCACCAGGCTCAGTCCCTGTCTCTCTGCCTCTGACT CAGGAGAGGAGGGGGTGCTGGACCCAAGGCTCCCTGTCTCTCTGCCTCTGACT CTCTCCTGATGGTGGCCCCTCTG[T/G]GCTCTCTCTCCGGTCGGATC
WI-7021b	112	G	A	::	TGGGGAGGACAGGGAGGAGATGCTGCAGTTCCAAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCCAAAT[G/A]CCCGACTGCCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACAGCCAATCAATTAATCAAACC ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A	G	::	TGGGGAGGACAGGGAGGAGATGCTGCAGTTCCAAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCC[A/G]AATGCCCGACTGCCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACAGCCAATCAATTAATCAAACC ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C	T	::	GGCAGTAGGAGGACCACCAGTGTGGGGTTCTGCTGGGAGAGCCTGCATCCCAGGATGCGGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACGAGCGCTAAACGTTGGTGA[C/T]GGTTGGGGAGCCTCT GGGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C	T	::	GGCAGTAGGAGGACCACCAGTGTGGGGTTCTGCTGGGAGAGCCTGCATCCCAGGATGCGGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACGAGCGCTAAACGTTGGTGA[C/T]GGTTGGGGAGCCTCT GGGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A	C	::	AATTCGCTGAAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAAATAGCATT[A/C]TCTTATCTTTTTTATCTGGTTCTATATGAATGCTAT ACATATTATTTCATTGGTCTTCTTCTTCTAACATCTTAGAG
WI-7091	153	A	C	::	AATTCGCTGAAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAAATAGCATT[A/C]TCTTATCTTTTTTATCTGGTTCTATATGAATGCTAT ACATATTATTTCATTGGTCTTCTTTTTTTATCTGGTTCTATATGAATGCTAT

Name	Pos			Sequence
WI-7136	58	T	C	TGTGAAGCCACATTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTTATTGAACTGT[T/C]AATTC TCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAGGACAGCAGCAACATGAAAGAGCATCAATGTG GTGGAGAAAGGGAAGGGGTTGGCTTTTAATTATTTTCTTCATCTTTATAACAAGAAAGNNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTTCTATATATG
WI-7146c	210	A	G	GGGACGCCTGTGTTGTTTGGCTCAATTGGGTTGTTGGTCACATGGAGCTCTTCCATTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCCGTGTCTCTCCTTGTGCCCCCAAGCCCATGCCCTGCCG TGGTTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCAACATGATGTGTGCCCCTCCTCCGCATGCC AACGC[A/G]GTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210	A	G	GGGACGCCTGTGTTGTTTGGCTCAATTTGGGTCACATGGAGCTCTTCCATTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCCGTGTCTCTCCTTGTGCCCCCAAGCCCATGCCCTGCCG TGGTTGGCAGCTGGGGCTGTGGGATGGGAGGGGTCCCAACATGATGTGTGCCCCTCCTCCGCATGCC AACGC[A/G]GTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202	G	A	GGGACGCCTGTGTTGTTTGGCTCAATTTGTTGGTCACATGGAGCTCTTCCATTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCCGTGTCTCTCCTTGTGCCCCCAAGCCCATGCCCTGCCG TGGTTGGCGAGCTGGGGCTGTGGGATGGGAGGGGTCCCAACGAGTGTGTGCCCCTCCTCCGCAT[G/A] [CCAACGCAGTTCATGTACAAGGCCCCTGCAACTGGAGAGAAAATTA
WI-7153	161	A	T	ATATTACAAACTTGCTTTTAGCTGATCTTCCATCCTCAAATGACTCTTTTTCTTTATATGTAACATA TATAAAATGGCAACTGATAGTCAATTTGATTTTATTCAGGAACTATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNNNN[A/T]AAAAAAAGTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTAAAGTATAGTACATTTACATATGTAAATGGTATGTT
WI-7155	156	T	G	TAGAATAGATGCGGTCATATTCTTCTTGGCTTCTGTCTTTCTTGGCTTCCTTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAACACCAGCTGCGCCCTACCCTATAATGATCCTGTGTCCTAAATTAATATACAC CAGTGGTTCCTCCTCCTG[T/G]TAAAGACTAATGCTCAGATGCTGTTTACGGATATTTATATTCTAG TCTCACTCTCTGTCCCACCCTTCTCTCTCTTCCCAACTCCAG
WI-7169b	161	A	G	AGCTCCACCAGATGCAGATTTGTGTTTGTTTCTTGTTATCACTGTCACACAGCTTATAACATGTAT GCTTTTCAGAATACAGTTGTCTAGCCAAGCCATCAAGTGTCTGAAATTCAATATTGGTTTATGCAAAT ACAGCAAACTTTATTTAAGTAGAT[A/G]GGAGAATATGTTAAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATTCTCAAATGGAAGTGTTATATATA
WI-7175b	194	C	T	CTCCTAGACTAGTGCTTACCTTATTAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAAATGGTTTACTGTCGTTCTGTCCATGCCTA[C/T]AGAT AATTTATTTTGTATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG

ID	Pos	Allele	Allele	Sequence
WI-7175	194	C	T	CTCCTAGACTAGTGCTTACCTTATTAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAGAAGTCAGTTGGAGAAAATGAAGAAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTCAGTTGACAAATATATAAATGGTTACTGCTGTCATGTCCATGCCCTA[C/T]AGAT AATTTATTTTGTATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273	G	A	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGCTACTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCCAGAAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7178	273	G	A	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCCAGAAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7182b	116	A	C	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACCAGTTCCTCTGCAACCCACTCTGAGCCT[A/C][T]CTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7182	106	C	A	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTATTCACCAGTTCCTCTGCAACCCA[C/A][T]CTGAGCCTATCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTCAGCTCAAGAGATGCCTTAAGATAATATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7191b	273	T	A	ATAATTGCTTGTTTCTAGCCTGGCAAGATATTTCATAAAGAGGGATAAACAATGCTGATTACTAC CTTTAAAAATATTTAGATAAATGCACAGCACCACCATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTAAAGCTTCTATTAAATTGTAAATTGTAAGCTTTGGCATATTTAAGGAG CTCCCAAAATGTGTTACCTATTAAATTGTAACTCAGCAAGTAGAAGACCATTT
WI-7199c	112	T	C	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCTTCCCGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTGGTACCCACCGTCCTTGACCTATGAGC[T/C]GGGGCCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTTTGGTGTCTGAATTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCGTCTAA
WI-7199b	112	T	C	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCTTCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTGGTACCCACCGTCCTTGACCTATGAGC[T/C]GGGGCCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTTTGGTGTCTGAATTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCGTCTAA

ID	No.	Allele	Allele	Sequence
WI-7216c	237	T	C	TGACACTAACACTCTAATTCAAGCGGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTCTCCCC AAGGACAAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAACTAAAATTGACTGTACTGTATGT TTAAAAACCCTTCCTGCTATACATAGGAAAAGACACATCCACCTAAAATTGACTGTACTGTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTG[T][T/C]CTTGTAATCACTT
WI-7216b	237	T	C	TGACACTAACACTCTAATTCAAGCGGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTCTCCCC AAGGACAAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAACTAAAATTGACTGTACTGTATGT TTAAAAACCCTTCCTGCTATACATAGGAAAAGACACATCCACCTAAAATTGACTGTACTGTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTG[T][T/C]CTTGTAATCACTT
WI-7220b	147	A	T	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTTGTCTCTTTAAGCTGGCAAACCCA TCATTAAATAGCACATAAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAGTAATCAATGGGCA GTGGCACTAGAA[A/T]AATCTTGAGCACAGTGAATGACCTATCCTGCAAACATCTAATGGATCTCTA AAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTTAGTGTGTT
WI-7220	140	A	T	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTTGTCTCTTTAAGCTGGCAAACCCA TCATTAAATAGCACATAAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAGTAATCAATGGGCA GTGGC[A/T]CTAGAAAAAATCTTATAAAATTCTGGCTTACTGCACATATTTAGTGTGTT AAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTTAGTGTGTT
WI-7226	232	C	-	GATCGAATTTTCAGATGATTCGGGAAATTTTCATTCAGGTATTTGTAATAGTGACTATATATGTATA TACATATCACCTCCTATTCTCTTAATTTTGTTAAAATGTAACTGGCAGTAAGTCTTTTTGATCATT CCCTTTTCCATATAGGAAAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT
WI-7228b	254	G	A	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCACCAGGAGATTACAATTTTTGCTCTTCTTGTGTAATCTATTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGGATCAGAAGATATCTTTGTGCCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAATGT[
WI-7228a	163	G	A	ATAGCTTCCAGATTACAACAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCACCAGGAGATTACAATTTTTGCTCTTCTTGTCTTGTAATCTATTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGGATCAGAAG[G/A]ATATCTTTGTGCCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAA
WI-7233c	213	C	T	CGATCGTACTGCCAGTAGCATTGTGTCGTCGTCCGGTCTTGTTTGTACATTCCATTTCAATTGTTACA GATGTGAACTTATTCCTTGTCACTAATTATTTAAAATTATTTCTAGGAAGTCAAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTTGCCACCTTTTGTGGCAATATTAAAGTGAACTGCTAATA GTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGGGCCTG

WI-7233b	213	C T	---	CGATCGTACTGCCAGTAGCATTGTGTCTGTCTGTCGGTCTCTGTTGTGTACATTCCATTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATATTTAAAATTATTTCTAGGAAGTCAAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAACTGCTAATA GTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGGGGCCTG
WI-7233	211	T C	---	CGATCGTACTGCCAGTAGCATTGTGTCTGTCTGTCGGTCTCTGTTGTGTACATTCCATTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATATTTAAAATTATTTCTAGGAAGTCAAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAACTGCTAATA GTGTAAGT[T/C]ACGTGCACAAAACCACTGCCAGATAACCAGAGGGGCCTG
WI-7238	128	T C	---	GCGTCTACAGACAGCTCACCATTTGTCCTGTATCTGTAAACACTTTTGTCTTTTGTCTTTTTCTTG TAAAATTGATGTTCTTTAAAATCGTTAATGTATAACAGGGCCTTATGTTTCAGTTGTTT[T/C]CCGTT CTGTTTTAAACAGAAAAATAAAAGGAGTGTAAGCTCCTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAAGAAACATTCAGTAGAACATTTTATTGCCTA
WI-7252f	520	T C	---	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCACTCGCAGCACGCCGGGGACACAGAG GCCTGCCCGGCCGGCGGCCCAGCCCCGGCCCTGGAGGCTGCCCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCGCCCTAGAGCCTGAGGTGGAACTCAGTCATTAGACTCCTCCTCCA CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252e	552	T C	---	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCACTCGCAGCACGCCGGGGACACAGAG GCCTGCCCGGCCGGCGGCCCAGCCCCGGCCCTGGAGGCTGCCCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCGCCCTAGAGCCTGAGGTGGAACTCAGTCATTAGACTCCTCCTCCA CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252d	540	T C	---	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCACTCGCAGCACGCCGGGGACACAGAG GCCTGCCCGGCCGGCGGCCCAGCCCCGGCCCTGGAGGCTGCCCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCGCCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252c	552	T C	---	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCACTCGCAGCACGCCGGGGACACAGAG GCCTGCCCGGCCGGCGGCCCAGCCCCGGCCCTGGAGGCTGCCCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCGCCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252b	540	T C	---	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCACTCGCAGCACGCCGGGGACACAGAG GCCTGCCCGGCCGGCGGCCCAGCCCCGGCCCTGGAGGCTGCCCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCGCCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA

ID	Pos			Sequence
WI-7252a	520	T	C	CCACCAGGAGGATCCCAGGCCAGCCCCTTCCCACTCGGACGAGACGCGGGGACGAGAGGCCTGCCCGGCGGGCCGCCGCCCCGGCCCCCGCGCCCCCTCGGTCTCTGGTCTCGGTCCGGACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAGCTCTCCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTTTTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAAATATAACGATCTCTTAAAAATACCACAGTTTGTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT[T/
WI-7265l	231	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTTTTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTTGTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTCTTTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT
WI-7265k	121	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTTTTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTT[T/G]GGTTCATTGTAAAATATAACGATCTCTTAAAAATACCACAGTTTGTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT
WI-7265j	174	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTTTTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGT[T/A]TATTATGTAAAATATAACGATCTCTTAAAAATACCACAGTTTGTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT
WI-7265i	227	T	C	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTTTTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTCACCCATTCTGTGGTTCATTGTAGTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATTATGTAAAATATAACGATCTCTTAAAAATACCACAGTTTGTATTTTT[T/C]CTTAAGGAGTAAAGATTTGCCT
WI-7265h	80	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTTTTTCCAGTATGT[T/A]TATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTTGTTTAAGGAAACCAAGCATATAGATGCATTAGTGTTTGTTTATTATGTAAAATATAACGATCTCTTAAAAATACCACAGTTTGTATTTTTCTTAAGGAGTAAAGATTTGCCT
WI-7265g	170	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTTTTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTTTAAGGAAACCAAGCATATAGATGCATTAGTGATT[T/G]TGTTTATTATGTAAAATATAACGATCTCTTAAAAATACCACAGTTTGTATTTTTCTTAAGGAGTAAAGATTTGCCT

WI-7265f	231	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAAACCAAGCATATAGATGCATTTGTTTATATTATTATGTAAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTTTCTT[T/A]AAGGGAGTAAAGATTTGCCT
WI-7265e	227	T	C	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTTT[T/C]CTTAAGGGAGTAAAGATTTGCCT
WI-7265d	174	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAAACCAAGCATATAGATGCATTAGTGATT[T/G]TGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265c	170	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAAACCAAGCATATAGATGCATTAGTAGTGTTGTT[T/G]GGTTCATTGTAGTTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265b	121	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTA GTTTAAGGAAAACCAAGCATATGATGCATTAGTAGTGCATTAGATGCATT[T/A]ATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265a	80	T	A	GATCACCCCAGCCACAAGCCCTTCGAGGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGGCCTGCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGGGCATCTCAGACTCAGACTCCTTGGCAAAAAACGGAGTCCGCAGGCCGCCAG GTGTTGTTGAAGACCACTCGTTCGTGTGGTCCTGCAAGAGGCCTCCTC
WI-7281b	183	C	—	GATCACCCCAGCCACAAGCCCCACCATGCCCCTATACCATGGCCCCTATACCATGGCCCCTATACCATGGCCCTGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGGCCTGCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC[C/A]TTGGCAAAAAACGGAGTCCGCAGGCCGCCAG GTGTTGTTGAAGACCACTCGTTCGTGTGGTCCTGCAAGAGGCCTCCTC
WI-7281	171	C	A	GATCACCCCAGCCACAAGCCCCACCATGCCCCCTATACCATGGCCCCTATACCATGGCCCCTGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGGCCTGCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC[C/A]TTGGCAAAAAACGGAGTCCGCAGGCCGCCG CAGGTGTTGTTGAAGAGACCACTCGTTCGTGTGGTCCTGCAAGAGGCCT

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WI-7282b	159	G	C	TGTCACCTGGCACATTCATTTTCTCAGTTGAAGAAGAGAAAAATTTGAAGAAGAGAAAATGTCCTTATGCTTTAGAGTTGCAACTTAAGTATATATTGGTAGGTGAGTGTTCCACTCAACTTNNNNNNNNNTAGGCCCTTTCATAAAAACCAAACT[G/C]TAGCAAGATGCAAATCTGTCGGTCTCCAGTTGGTTATCTGAATAGTGTCACCAAATTCCACCAAGACAGTGCTGAGATTGG
WI-7292	92	T	C	CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGCTCCCCAATTATATCTCCCCACTCCACTACTCTCTCCTCCACTTCATTTCC[T/C]TGTCCTTCTCTCTCTAATTCAGTGTTTTGGAGGCCTGACTTGGGGACAACGTATTATTGATATTATTGTCTGTTGTTTCCTTCTTCCCAATAGAAGAAAAGTCATGGAGCCTGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A	G	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAAACCAAGGTGGTGGATAATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG[A/G]CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAAATCAAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCGA
WI-7301e	94	T	G	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAAACCAAGGTGGTGGATAATGGTGGCGGTG[T/G]TGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAGAAGCTCGGGCAGTCAAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301d	138	A	G	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAAACCAAGGTGGTGGATAATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGACGGT[A/G]GTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCATCAAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301c	211	A	C	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAAACCAAGGTGGTGGATAATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCAAATTATGGACAC[A/C]CATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301b	182	C	T	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAAACCAAGGTGGTGGATAATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTA[C/T]AGTGGACAACAGCAATCAAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301	88	G	T	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGACCAGGATATGGAAACCAAGGTGGTGGATAATGGTG[G/T]CGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCAAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG

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WI-7301	205	A C	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAAATTTTGA CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTGGAAAATTACAGTGGACAACAGCAATCA AATT[A/C]TGGACACATGAAAAGGGGGCAGTTTGGTGGAAGAAGCTCGGGCAG
WI-7314c	49	G A	CTCTCCTTTTTTCTTCAGATCTGCTCCTGGGTTTAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGGGTCCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAAATGTGTAGTCTACCTTTATTTTTTATTAACAAAACTTGTTTTT
WI-7314b	49	G A	CTCTCCTTTTTTCTTCAGATCTGCTCCTGGGTTTAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGGGTCCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAAATGTGTAGTCTACCTTTATTTTTTATTAACAAAACTTGTTTTT
WI-7314	36	A G	CTCTCCTTTTTTCTTCAGATCTGCTCCTGGGTTTA[A/G]TTGGGAGGTCAGTTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGGGTCCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAAATGTGTAGTCTACCTTTATTTTTTATTAACAAAACTTGTTTTT
WI-7321b	199	C T	ACTCAGGGAAGGAAGGGGATGCCCCATTAAAGTGACAAAGGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCCTGACAGTCAAGGGACTGCTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCCAAGACTGGAGNNNNNNNNAGGGTGGCACACCCATC[C /]TGTTTGCTGGGGTGTGGCAGCCACATCCAAGACTGGAGCAGCAGCAGGCTGGCCA
WI-7321	199	C T	ACTCAGGGAAGGAAGGGGATGCCCCCATTAAAGTGACAAAGGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCCTGACAGTCAAGGGACTGCTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCCAAGACTGGAGNNNNNNNNAGGGTGGCACACCCATC[C /]TGTTTGCTGGGGTGTGGCAGCCACATCCAAGACTGGAGCAGCAGCAGGCTGGCCA
WI-7336b	248	A C	AGACATTCTCGCTTCCCTGAAAGACTGAAGAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAACTTGGGCACATGCCAATGATAGGTCCAGAAGTTCCTTATGTTAAGCCCTGGCAG GCAGGTGTTATTAAAAAATTCTGAAATTTGGGGATTTTCAAAAGATAATATTTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGCAGCAACTAGAAATCA[A/C]CA
WI-7338c	221	A G	CTCTTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACAGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAACAAAGAAACAGAATCAATATATAATATTTACAGACTATCTGCAGCTA GTGTGTGTTTCTTCTTACACAC[A/G]TATACACACAGAGACATCCAGAAAATTCTGTT

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WI-7338b	125	A	C	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAAGAAACAGAATCAATATATCACACAGACTATCTGCAG CTAGTGTGTTCTTCTTACACACAGAAAATTCTGTT
WI-7338	125	A	C	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTGAGC CATTATTTGTGTCAGAGAACAAAAGAAACAGAATCAATATATCACACAGACTATCTGCAGCTA GTGTGTTCTTCTTACACAC[A/G]TATACACACAGAAAATTCTGTT
WI-7338	221	A	G	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAACTTAAAATACCATTAAAATACATTTGTATTCATTGTGAACAGGTATTCTTCA CAGATCTCATTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACACTTAAGAAATTTGAGCAGAATTAAAAAGAA
WI-7384c	146	T	A	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAACTTAAAATACCATTAAAATACATTTGTATTCATTGTGAACAGGTATTCTTCA CAGATCTCATTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACACTTAAGAAATTTGAGCAGAATTAAAAAGAA
WI-7384b	146	T	A	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAACTTAAAATACCATTAAAATACATTTGTATTCATTGTGAACAGGTATTCTTCA CAGATCTCATTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACACTTAAGAAATTTGAGCAGAATTAAAAAGAA
WI-7384	145	T	A	---	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7388c	106	A	T	---	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7388b	106	A	T	---	

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WI-7388	94	T	A	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTGTAGCTGGTTTATTTTTACTTTGCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAG[T/A]CTGAAGCGACTATAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7438	64	A	G	TTAGATTTAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCCAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAACCCTATTGGAACCAAGTCTTCAGATTGTNCCATGTGCAGACAGGCTCCT TGTCTGTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACTGTTAACATAGTTTGTNCTGGTATTTGTTA TTGGAAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152	T	C	CCATGATCCCCTCCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAAACAAGCCCAAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCT[T/C]TGTTGTTAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7454	152	T	C	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAAACAAGCCCAAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCT[T/C]TGTTGTTAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7464c	177	G	C	AATTTGAAAATCTGAAAAAAAGTCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTTAACCATGTACAATCTAAATTATAATTCTATGTA CAACAGAGCCACAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACTCAT[G/C]CCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464b	168	C	A	AATTTGAAAATCTGAAAAAAAGTCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTTAACCATGTACAATCTAAATTATAATTCTATGTA CAACAGAGCCACAGCCCTTAACAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464a	103	C	A	AATTTGAAAATCTGAAAAAAAGTCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTTAACCATGTACAATG[C/A]ACTAAATTACTATTTATAATTTCCTAT GTACAACAGAGCCACAGCCACAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7499b	134	T	G	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAAACCATTCCAGACAAACTTCCACTTCGAAGGTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTCA[T /G]TATAGTCCTCTTCATTTAGCATCAGTCAGTGAGGCAATACACTGCCATCATGATCCCTTTTTTAGGA ACTCTGTACAAATTCCCTTTGAAAATATAAATTTGAAAATGAGTGATGA

ID	Pos			Sequence
WI-7499a	33	A	G	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAAA[A/G]CCATTCCAGACAAACTTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAATTCCCTTTGAAAATATAAATTTGGAAATGAGTGATGA
WI-7506b	118	A	C	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAAAGTAGTCCTGGTGCTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAGTGAGTGAAGAGGAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACTCTGTTCTACCATCCCTACCCACT
WI-7506	118	A	C	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAAAGTAGTCCTGGTGCTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAGTGAGTGAAGAGGAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACTCTGTTCTACCATCCCTACCCACT
WI-7534b	143	C	T	TGTGAATTCTTAGCTCTGGAAGGTGTTATGCCTTTGCGGGGTTCTTGATGTGTTCGCAGTGTCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCCCGGTGATAGAATTGCT AAATTGT[C/T]GTGAAATAGGTTAGAATTTTCTTAAATATGGTTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAATTGGATTGGTGTGATCTTTTTGGTAGTTGTAATTT
WI-7534	135	T	C	TGTGAATTCTTAGCTCTGGAAGGTGTTATGCCTTTGCGGGGTTCTTGATGTGTTCGCAGTGTCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCCCGGTGATAGAATTGC[T /C]AAATTGTCGTGAAATAGGTTAGAATTTTCTTAAATATGGTTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAATTGGATTGGTGTGATCTTTTTGGTAGTTGTAATTT
WI-7543b	162	G	A	GGGAAAGAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCTCCTTG[G/A]GGAAGACCCAGCTTGCAGTGACAGCTTGAGTGAGTCAGTTA CTCTGCCAGCCCTCAGATTATTTTCCTCTGGCTCCTTGGATGATGTAGTCAGTTA
WI-7543	162	G	A	GGGAAAGAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCTCCTTG[G/A]GGAAGACCCAGCTTGCAGTGACAGCTTGAGTGAGTCAGTTA CTCTGCCAGCCCTCAGATTATTTTCCTCTGGCTCCTTGGATGATGTAGTCAGTTA
WI-7555c	60	T	C	GGTGATCAAGATCGTTCCACAGGGCTAATGCCACCATCCCCTCAAAATTTGTAGAGG[T/C]TCTA AAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGAAGTAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCATTTGAATTTCAG

WI-7555b	60	T	C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTAAAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTTGGGTCATAAGAAGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGTATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTGAATTTCAG
WI-7555	60	T	C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTAAAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTTGGGTCATAAGAAGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGTATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTGAATTTCAG
WI-7567b	290	G	T	TGAGCCATCACTAGAAGAAAAGCCCATTTCAACTGCTTGAAACTTGCCTGGGGTCTGAGCATGATGGGAATAGGGAGACAGGGTAGGAAAAGGGCGCCTACTCTTCAGGGGTCTAAAGATCAAGTGGGCCTTGGATCGCTAAGCTGGCTCTGTTTGATGCTATTTATGCAAGTTAGGGTCTATGTATTTAGGATGCGCCTACTCTTCAGGGGTCTAAAGATCAAGTGGGCCCTTGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63	T	C	AATGTATCCCCTTTCGGTCCAACAACAGGAAACCTGACTGGGGCAGTGGGCCAGTGAAGGAAGGGATGGCA[T/C]AGCCGTTATGTGTAAAAAAACAAGTATCTGTATGACAACCCGGATCGTTGCAAGTAACTGAATCCATTGCGACATTGTGAAGGCTAAATGAATGGGAAATAGCGTTGTTATGCGCCTTGGGTTTAAATTATTTGATGAGTTCCACTTGTATCATGGCCTACCCGAGGAGAAGAGGAGTTTG
WI-7574c	216	A	G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTGTTTGTTGTTGCCAAGGCCAAACTCCCACTCTCTGCCCCCCTTTAATCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTTGTACCACTTACATTTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTGATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTCATCCCGTTA
WI-7574b	216	A	G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTGTTTGTTGTTGCCAAGGCCAAACTCCCACTCTCTGCCCCCCTTTAATCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTTGTACCACTTACATTTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTGATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTCATCCCGTTA
WI-7574	216	A	G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTGTTTGTTGTTGCCAAGGCCAAACTCCCACTCTCTGCCCCCCTTTAATCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTTGTACCACTTACATTTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTGATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTCATCCCGTTA
WI-7576c	168	A	T	AATGATGATAATGATGATGACGACGACGACAAGCAGATGATGCTTGTAACAAGAAAACATAAGAGAGCCTTGGTTCATCAGTGTTAAAAATTTTGAAAAGGCGGTACTAGTTCAGACACTTTGTGAAGGCCTTATTCTACATTTCACCTACTTTGTTGGTAAGTGAGAGACAGACAAGCAAANNNNNNNNAAGAAAAAATAAAC

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WI-7576b	168	A	T	AATGATGATGATAATGATGATGACGACGACGACGATGATGCTTGTAACAAGAAAAACATAAGAGAGAGCCTTGGTTCATCAGTGTTAAAAAATTTTGAAAAGGGCGGTACTAGTTCAGACACTTTGGAAGTTTTGTGTTCTGTTGTTAAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCTTATTCTACATTCACCTACTTTGTAAGTGAGAGAGAGACAAGGAAGCAAGAAGCAAANNNNNNNNAAAGAAAAAAATAAAC
WI-7577q	77	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAACATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAAATATGCA[T/C]CAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAGAGAAGTTCATTTGGTTACACGTAGGAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50	G	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAAGAAGTTCATTTGGTTACAC[G/A]TAGGAAGAAGAAGCATCAAAGTGGAGATGGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577o	157	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATA[A/G]AGTGTTTGCTTTCCTTTAAAAATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAAGAAGTTCATTTGGTTACACGTAGGAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577n	48	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAAAAATATGCATCAAATC[G/A]TCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAAGAAGTTCATTTGGTTACACGTAGGAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577m	84	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAAAAATATGCATCAAATCGTCTCTCATT[T/C]ACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAAGAAGTTCATTTGGTTACACGTAGGAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577l	93	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAAAAGAAGTTCATTTGGTTACACGTAGGAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577k	154	C	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAAGAAGTTCATTTGGTTA[C/A]ACGTAGGAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC

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WI-7577j	117	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577i	77	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAA[G/C]TGTTTGCTTTCCTT AAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577h	50	G	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTACAC[G/A]TAGGAAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577g	157	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACAT[A/G]AGTGTTTGCTTTCCTT AAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577f	48	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577e	84	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATT[T/C]ACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577d	93	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577c	154	C	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTA[C/A]ACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC

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WI-7577b	117	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTGAGGGTTTAGTA[A/G]ACAGTAGGAGGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577	107	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCATCAAATCGTCTCTCATTTTCTGAG[G/A]GTTTTAGTAAACAGTAGGAGGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7619q	106	C	G	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACT[C/G]TCGTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGGAGTGTGGGGTCTGTCTCTCCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAAACATACGAGAAACCTATTC
WI-7619p	150	T	C	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCGTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCCT[T/C]CTAAGGGGGAGTGTGGGGTCTGTCTCTCCCCTTTTTCCATCTTTTTCCT CTCGCTTTCTTTCTTACACAGAAAACATACGAGAAACCTATTC
WI-7619o	228	A	G	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCGTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGGAGTGTGGGGTCTGTCTCTCCCCTTTTTCCATCTTTTTCCT CGCTTTCTTTCTTACACAGAAAACATA[A/G]CACATACGAGAAACCTATTC
WI-7619n	237	G	C	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCGTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGGAGTGTGGGGTCTGTCTCTCCCCTTTTTCCATCTTTTTCCTCT CGCTTTCTTTCTTACACAGAAAACATACATACC[G/C]AGAAACCTATTC
WI-7619m	99	C	T	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTCCCTAA[C/T]GAGACTCTGTGTGCTGGGGGTGCTAATTACA TGGCAGGAAGAATGGGGCCTCTAAGGGGGAGTGTGGGGTCTGTCTCTCCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAAACATACGAGAAACCTATTC
WI-7619l	189	T	A	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTGTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTGTGGGGTCTGTCTCTCCCTTTTTCCA[T/A]CTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAAACATACACGAGAAACCTATTC

ID	Pos			Sequence
WI-7619k	90	C	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCC[C/G]CTCCCTAAGCGACTCTCTGTGTCTCCCTTTTTCCATCTTTTTCCT ATGGCCAGGAAGAATGGGCCCTCTAAGGGAGTGTGGGGTCTGTTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206	T	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGACT[C/G]TCTGTGTCTCCCTTTTTCCATCTTTTTCCT ATGGCCAGGAAGAATGGGCCCTCTAAGGGAGTGTGGGGTCTGTTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC CGC[T/G]TTCTTCT
WI-7619i	106	C	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGACT[C/G]TCTGTGTCTCCCTTTTTCCATCTTTTTCCT ATGGCCAGGAAGAATGGGCCCTCTAAGGGAGTGTGGGGTCTGTTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150	T	C	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGACTCTCTGTGTCTCCCTTTTTCCATCTTACATGG CAGGAAGAATGGGCTCTAAGGGAGTGTGGGGTGCTAATTACACATGG TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC CTT[T/C]CTAAGGG
WI-7619g	228	A	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGACTCTCTGTGTCTCCCTTTTTCCATCTTTTTCCTCT CAGGAAGAATGGGCCCTCTAAGGGAGTGTGGGGTCTGTTCTCTCCCTTTTTCCATCTTTTTCCTCT CGCTTTCTTCTTACACAGAAACAT[A/G]CACATACCGAGAAACCTATTTC
WI-7619f	237	G	C	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGACTCTGTGTCTCCCTTTTTCCATCTTTTTCCTCTCT CAGGAAGAATGGGCCCTCTAAGGGAGTGTGGGGTCTGTTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACC[G/C]AGAAACCTATTTC
WI-7619e	99	C	T	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAA[C/T]GAGACTCTGTGTCTCCCTTTTTCCATCTTTTTCCTC TGGCAGGAAGAATGGGCCCTCTAAGGGAGTGTGGGGTGCTAATTACA TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189	T	A	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGACTCTCTGTGTCTCCCTTTTTCCATCTTACATGG CAGGAAGAATGGGCTCTAAGGGAGTGTGGGGTGCTAATTACACATGG TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC CCA[T/A]CTTTTTCCTC

ID	pos	a1	a2		Sequence
WI-7619c	90	C	G	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCGTGCTGGGGGTGCTAATTAC ATGGCCAGGAAGAAGAATGGGCGCCTCTAAGGGGAGTGTGGGGTCGTCTCTCCCTTTTCCATCTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACACATACCGAGAAACCTATTTC
WI-7619b	206	T	G	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCCTAACGAGACTCTCGTGCTGGGGGTGCTAATTACACATGG CAGGAAGAGAATGGGCGCCTCTAAGGGGAGTGTGGGGTCGTCTCTCCCTTTTCCATCTTTTCCTCTCT CGC[T/G]TTCTTTCTTACACAGAAACATACACACATACCGAGAAACCTATTTC
WI-7619	189	T	A	---	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCCTAACGAGACTCTCGTGCTGGGGGTGCTAATTACACATGG CAGGAAGAGAATGGGCGCCTCTAAGGGGAGTGTGGGGTCGTCTCTCCCTTTTCCA[T/A]CTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACACATACCGAGAAACCTATTTC
WI-7626d	105	A	G	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGC[A/G]TTAAACCACATCATGGACCAAATGTG CCATACTAATGAGCAATTAGCACAATTGAGACTGAAATTAGTACACTATGTTCCTTGGACTGTTCA CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTTGGACTGTTCA
WI-7626c	155	C	T	---	CCTTTGTATGTGGAAGTATACCTGGCTTTT[T/A]TTAAAATATGTATTTAAAAACAAAAGCAACAG TAATCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACATCATGGACCAAATGTG CCATACTAATGATGAGCAATTAGCACAATTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTTGGACTGTTCA
WI-7626b	28	T	A	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAAACAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACATCATGGACCAAATGTGCCA CCATACTAATGA[T/C]GAGCAATTAGCACAATTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTTGGACTGTTCA
WI-7626	144	T	C	---	TCCCATAACCGCTGATTCTCAGGGTCTCGCTGCGCCCCCAGATGGGGGAAAGCAACAGGTGGGC TTCCCAGTGGCTGCTGCCCAGCCCACCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCCTAAA[A /G]TAAGGGCAGAGTCACACTGGTGGCCACAAATAAAAATGGATTTATTTAGAATTTCATATGAC
WI-7689c	134	A	G	---	GATAATATTGTGGTGCCACAAATAAAAATGGATTTATTTAGAATTTCATATGAC

WI-7689b	134	A	G	---
				TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGCTTCCCAGTGGCTGCTGCTGCCCAGGCCCAGACCTTCTAGGACGCGCACCCAGGCCAGCTGATACAAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT[A/G]TAAGGGCAGAGTCACACTGGTGCCACAAATAAAATGGATTTATTAGAATTTCATATGAC
WI-7689	121	G	A	---
				TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCCCACCCAGATGGGGGAAAGCACAGGTGGGCTTCCCAGTGGCTGCTGCTGCCCAGGCCCAGCTGGGCAGCTGATACAAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT[G/A]GTTGTTCCTAAAATAAGGGCAGAGTCACACTGGTGCCACAAATAAAATGGATTTATTAGAATTTCATATGAC
WI-7690	45	G	A	---
				TGGAGAACATTCAATCTTGCCGTCACTATTCATCAATGAAGATTA[G/A]CACTGAGATCCAGAGAGGCTGGATGACTTGCTCAAGTTCACCAGCATGGTGGCAAAGAGAGGTCCAGAGTCCTGGCCCCTTGATGCCCAGCTCAGTGCCACAAAGCTCAGTGAGGAGGGATGTTCCAGTGGATGAGGGCCACCAGGAAGCACAGGTCCAAGGCTGGTCCCACACTTATCAGCAGCAACAACTGTCAGTTCATCC
WI-7703b	164	T	C	---
				ACAGAAAAGTTGAATTTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCACAGTGATCAAGTTATTTTAATTTGGTTTCACATTGGAAACAAGTCAGTCATTCAGATATGATTCAAATGTCTATAAACCAAACTGATGT[T/C]AAGTAAATGGTCTCTGTTTATTTAACCTCTAAATTCTTTCATTTTAGGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T	C	---
				TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCCGAGCCAAGGGTTCAGAGACTCAGGGCCCCAGCACTAAAGCACTAAAGCAGTGGAC[C/A]CAGGAGTCCCTGGTAATAAGTACTGTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGCGCTCATCCGAGGCAGGGTCAGGAGAGGGGCAGAACAGCGCGGTCCTGTCTGCCCAGCGCCAGCTCTCAGCC
WI-7743e	106	C	A	---
				TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCCGAGCCAAGGGTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGCGCTCATCCGAGGCCTCATCCGAGGCAGGGTCAGGAGGGGCAGAACAGCGCGGTCCTGTCTGCCCAGCGCCAGCTCTCAGCCAACG
WI-7743d	275	C	T	---
				TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCCGAGCCAAGGGTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CAGGAGTCCCTGGTAATAAGTACTGTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGCGCTCATCCGAGGCCTCGAGGCCAGCAGGGTCAGGAGAGGGGCAGAACAGCGCGGTCCTGTCTGCCCAGCGCCAGCTCTCAGCC
WI-7743e	106	C	A	---

				Sequence
WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGACCCCAGGAGCCTGGGGGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743e	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGCCAGCCAGCAGCCAGCTCTCAGCC GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743c	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743b	275	C	T	TTAAATGAGTGTGTTGTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	275	C	T	TGACATTTATTCAAAGTTAAAAGCAAACACTTACAGAATTATGAAGAGGTATCTGTTTAACATTTCC TCCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGGAGAGACATCAAGTG GAGAGAAATC[A/G]TAGTTTAAACTGCATTATAAATTTTATAACAGAATTAAAGTAGTACTGTG GATAAAATGTGTAATTTTGTTTATATTTCCCATTTGGACTGTAACTGACTGCC
WI-7758	144	A	G	

ID	Pos		Sequence
WI-7765b	126	G C	ACAGGGGCCTTGGCAGGTGCAGCCCCCACTGCCTGCCTTTGACCTGCCTGCCTCCCTTCATGCTGATGGAAATTCCT TCATCTGGAACCATCAGAAACACCCTCACACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGG GAAAACATTCCATCGTGAGTCAACTTGCTCCCTATCTTGCCACCCTCATGCTGTGTG ACTCAAACCAAATCACTGAACTTTGCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237	C G	TTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCCAGATTATTTTAAGTTTTATCCGTAGTTT GATAAAAGATTTCCTATTCCTTGGTCTGTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAAGGCA GACTAGGGTCATGTCTTTTACCCTTTNNNNNNNNTTGTAAAAGTCTAGTTGACCTACCTACTTTTCTTT GATTTCGACGTTTGACTAGCCATCTCAAGCAA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C	TGCAACCTCTTTTCGTGATGGGCAGCCTGCTGGTCAGCACTCCAGTAGGCGAGAGACGGCACCCAGAAT CAGATCCCAGCTTCGGCATTGATCAGACCAAAACAGTGCTGTTCCCGGGGAGGAAACACTTTTTTAA TTACCCTTTGCAGGCACCACCTTTAATCTGTTT[T/C]ATACCTTGCTATTAAATGAGCGACTTAAA ATGATTGAAAAATAATGTCTGTCCTTAGTAGCAAGTAAAATGTGTCTTGCT
WI-7785c	165	G	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNGCCAAGGCTAATCCAATTATTATTCACATTACCA TAATTTATTTGTCCATTGATGTATTTATTTGTAAATGTATCTTGGTGCTGC
WI-7785b	165	G	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCCCATTATTATTCACATTACCA ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAAGGCTAATCCAATTATTATTCACATTACCA TAATTTATTTGTCCATTGATGTATTTATTTGTAAATGTATCTTGGTGCTGC
WI-7785	156	- T	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANN[-/T]NNNNNNNNNGCCAAGGCTAATCCAATTATTATTCACATTTACCATAATTTATTTGTCCATTGA TGTATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84	G A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAAATGTGAATGAAGCTAATGTGAGTGAAGTGAATGTGAGTGAAGCTCCCTGCCCGGTGCCCTAGGATAT GCCCTCCTGGTGGTCTGGGGGGCGTGTCTCAGACGACTAGCCCAGGACCCATCT
WI-7789b	84	G A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAAATGTGAATGAAGCTAATGTGAGTGAAGCTCCCTTCAGCGCCCGGTGCCCTAGGATAT GCCCTCCTGGTGGTCTGGGGGGCGTGTCTCAGACGACTAGCCCAGGACCCATCT

WI-7789	73	G	A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGAGACTCTCCC TGACG[G/A]TGGAATTAAGTTTAGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAAGCTAATGTGAGTGAGCGACTGAGCTCCCTTCAGGCCCGCTGCCCTAGGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCCAGGACCCATCT
WI-7790b	190	C	T	AATTGTCAGTCACTTCTTCAAAACCTTACAGTCCTTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGTAGCTTTTTACTTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACTC[C/T]TTCTATACTTT AAGGATACTCTATTTTTAAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	C	T	AATTGTCAGTCACTTCTTCAAAACCTTACAGTCCTTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGTAGCTTTTTACTTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACTC[C/T]TTCTATACTTT AAGGATACTCTATTTTTAAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	C	A	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTTCTTTCTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAATTAATGATTAAAATAGCATGCCTTCTCTCTCTTCTCT TAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAATTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81	C	A	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTTCTTTCTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAATTAATGATTAAAATAGCATGCCTTCTCTCTCTTCTCT TAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAATTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41	G	A	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC TGTCTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGGATAAAATAAATGGGATTTTC TTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA
WI-7814b	41	G	A	TTCTCTCTCATTTTATCCCTCACCTGTA[G/A]CATGCCAGTCCCGTTTCATTTAGTCATGTGACCACTC TGTCTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGGATAAAATAAATGGGATTTTC TTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA
WI-7814	28	G	A	TTCTCTCTCATTTTATCCCTCACCTGTA[G/A]CATGCCAGTCCCGTTTCATTTAGTCATGTGACCACTC TGTCTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGGATAAAATAAATGGGATTTTC TTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA

WI-7830d	150	C	T	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTCTGTTAATAGTCATCACATTCTATGCCAAACAGGAACG ATCCATAAACTTTAGT[C/T]TAATGTACACATTGCATTTTTACTTTTTGCGTGTGGA AGGTTGATCGTTGTGTTGTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830c	54	G	A	---	GCAGGAAATAGTCACTCCCACTCCACATAAGGGGTTTAGTAAGAAGTCT[G/A]TCTGTCTGA TGATGGATAGGGGGCAAATCTTTTCCCCTTCTGTTAATAGTCATCACATTCTATGCCAAACAGGA ACGATCCATAAACTTTAGTCTTAATGCATTTGATACACATTAATTTGTTGTTTCCTTTG AGGTTGATCGTTGTGTTGTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830b	134	G	A	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTCTGTTAATAGTCATCACATTCTATGCCAAACAGGAAC[G/A]ATCCATAAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTTCCTTTG AGGTTGATCGTTGTGTTGTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830	44	A	G	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTA[A/G]GAAGTCTGTCTGTCTGA TGATGGATAGGGGGCAAATCTTTTCCCTTCTGTTAATAGTCATCACATTCTATGCCAAACAGGA ACGATCCATAAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTTCCTTTG AGGTTGATCGTTGTGTTGTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7865e	25	C	T	---	CCACTTCCTATCTGATTTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C	T	---	CCACTTCCTATCTGATTTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGGT ATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C	T	---	CCACTTCCTATCTGATTTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C	T	---	CCACTTCCTATCTGATTTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGGT ATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA

WI-7865	25	C T	---	CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGAGGGTGGTTGGGGTATGCTACTACTCATAAGATTTCAGGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAAATCACATGCCTATGTAAGGAAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191	C T	---	CCACTTCCTATCTGATTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGAGGGTGGTTGGGGTATGCTACTACTCATAAGATTTCAGGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAACCTGAAATCACATGCCTATGTAAGGAAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92	A C	---	TTCAAACACCTGTCTTCCACCCTCCCACCATCTGTGCAATCACTTCACCCTTCAGCCTCACTAGTCCCCCTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGGTTTAATATGGCCTGTTGAGTTTAATGTTGATTTTCTTTAAGTAACCATTCTGTCTTGCTATAAATCTATGTCTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92	A C	---	TTCAAACACCTGTCTTCCACCCTCCCACCATCTGTGCAATCACTTCACCCTTCAGCCTCACTAGTCCCCCTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGGTTTAATATGGCCTGTTGAGTTTAATGTTGATTTTCTTTAAGTAACCATTCTGTCTTGCTATAAATCTATGTCTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173	C T	---	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGGCTTAAAACCGGGCTTTCACCCAACCTGCTCCCTCTGATCCTCCATCTCCACGTCTCCAGTACTCCAGTACACAATCATTTAATATTTCCCTGTCTTCAAGCAA[C/T]TAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173	C T	---	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGGCTTAAAACCGGGCTTTCACCCAACCTGCTCCCTCTGATCCTCCATCTCCACGTCTCCAGTACACAATCATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAA[C/T]TAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66	T C	---	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGGCTTAAAACCGGGCTTT[T/C]TCACCCAACCTGCTCCCTCTGATCCTCCATCTCCACGTCTCCAGTACACAATCATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85	T C	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGGGTGGGGTGGCGGGAATCC[T/C]ATTTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAGCTGCAAATTGCCTGCAAAAATGAAATCCAATGAAATCGAAATCAGAGAATATTTAAAACATCATTACTGCCATCTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76	C	T	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATAACTCTGCAGTGATTGATTAGAAGGG GTGGGGTGG[C/T]GGGAATCCTATTTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAATATTTAAAACATCATTACTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54	C		TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGGCCGCTCTCCCCCTG CAGCCGGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGGCGGGCCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATTGAAATGGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCAAGGCTGTCTTCTCCCAGAGCACAGAAG
WI-7889b	54	C		TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGGCCGCTCTCCCCCTG CAGCCGGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGGCGGGCCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATTGAAATGGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCAAGGCTGTCTTCTCCCAGAGCACAGAAG
WI-7894c	142	A	G	AGCCCACCCCAAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTTGTACT TTTACTATATCTACATACACATCAATTAAACTTATGTCCTATTGTTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAAAATTTGCATTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATTCCATA
WI-7894b	142	A	G	AGCCCACCCCAAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTTGTACT TTTACTATATCTACATACACATCAATTAAACTTATGTCCTATTGTTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAAAATTTGCATTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATTCCATA
WI-7900e	84	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAAGACATTAAAAGAAATC
WI-7900d	128	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAAGACATTAAAAGAAATC
WI-7900e	84	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAAGACATTAAAAGAAATC

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WI-7900d	128	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCTGCCATTGAAACAGTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAACTCAACTATAGAAGACATTAAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGAGTACATTCTCTCAGATTTGAACCAGTGAAA AAAATGCATTGATCATGAATAGGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900c	84	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900b	128	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGATTGAAACAGTGATTAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900	84	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7901c	33	C	T	AGACTTAGGTACAAATTGCTCCCCTTTTTATATA[C/T]AGACACACACAGGACACACATATATTAAACAG ATTGTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGGTTATTGGGCGCAGCGCCGTGGTCGT CAC[C]CAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33	C	T	AGACTTAGGTACAAATTGCTCCCCTTTTTATATA[C/T]AGACACACACAGGACACACATATATTAAACAG ATTGTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGGTTATTGGGCGCAGCGCCGTGGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT

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WI-7901	33	C	T	AGACTTAGGTACAATTGCTCCCCTTTTTATATA[C/T]AGACACACACAGGACACACATATATTAAAACAG ATTGTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTCGCTCTGTCATACAGACAGGTAACCTAGTTCT CACTCAGTGCGCTCTGCGATGCTCTGCGATGCTCTGT
WI-7901	271	T	G	AGACTTAGGTACAATTGCTCCCCTTTTTATATACAGACACACACAGGACACACATATATTAAAACAGATT GTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAAACATGGTAAGACCCT TTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTCGCTCTGTCATACAGACAGGTAACCTAGTTCTCAC TCAGTGCGCTCTGCGATGCTCTGTCATACAGACAGGTAACCTAGTTCTGTCATACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150	C	A	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTAATACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28	A	T	CATTCCGCATCTGTCAACCAGGACAGAA[A/T]GCATGGACAAGGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTC ATTTACAATGCAATACTTACATTTAATACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150	C	A	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTAATACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203	G	T	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCCACAAGCAGCCAGCACCCACAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCAGCCGAGCCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACGACTATGGGCAGCCCAGTGCTGCCACCTG GA[G/T]TCTCTCCCTGGAGCAGCAGGTCAAAAAGGCCAACAACCCACAAGCAGCCAGCACCCACAAGGCCAGGTCCTG
WI-7947	203	G	T	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCCACAAGCAGCCAGCACCCACAAGGCCAGGTCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCAGCCGAGCCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACGACTATGGGCAGCCCAGTGCTGCCACCTG GA[G/T]TCTCTCCCTGGAGCAGCAGGTCAAAAAGGCCAACAACCCACAAGCAGCCAGCACCCACAAGGCCAGGTCCTG
WI-7963b	145	T	C	CATGTGCTGCATGAAGAGCTAATTAAAAAAGCAAAGTAAGACTAATTATTTAAAATAAAAAATGCC ACAAATTTCATTTCATTTCCTTCTAAGTATTACAATGGAGTTTATTCTGCCTAAAAAGTGGAAGAAAT TGAGTGAATGA[T/C]AATTTGTAATTTAGGATAAGATCCAAGTTATTTCCCCAACTCTGTTTCCC CCATAAAAGTTAGGCATGAGGGAGGAGCACTCATTAAAGGCAGAAGACGGAAAA

WI-7972c	268	T	G	GGAGTTCTGGTTCCTACTGGGGCCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCGTGTCAGCCATTCCTGTCGTCCCATGAGATGATGCCATGGGTCTCAGCAGGGGAGG GTAGAGCGGGAGAAAGGAGAACCAAAAAGAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGAGATCC
WI-7972b	268	T	G	GGAGTTCTGGTTCCTACTGGGGCCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCGTGTCAGCCATTCCTGTCGTCCCATGAGATGATGCCATGGGTCTCAGCAGGGGAGG GTAGAGCGGGAGAAAGGAGAACCAAAAAGAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGAGATCC
WI-7972	268	T	G	GGAGTTCTGGTTCCTACTGGGGCCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCGTGTCAGCCATTCCTGTCGTCCCATGAGATGATGCCATGGGTCTCAGCAGGGGAGG GTAGAGCGGGAGAAAGGAGAACCAAAAAGAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGAGATCC
WI-7981	261	T	G	AACCCCTGAAATCGGAAATGGAAGGGACTTCCTCTTCTCTCCCTGTTTAAATTATAAGATGTCAT CCCCTTGTGTCAGATGACAGACCCCTGGCTTTGCTTGGCCAGAGAGGACCCCACTGGACTGGGTTTG TCTCTGCATCTCATTGTAGAGCTTGGTGGCTGAGCTTCCCATTGGTCTCTCCTAAAACAT AGGATTGTTCACATGCCATCATAACCATTCCCATTGGTCTCTCCTAAAACAT
WI-7992b	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAACTGCTTGAATATNCCAGATTTGTTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTTCTTCACGAAAATAAATTGCTATCAAGAGCAAAC TATGAACAATTATTATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGGGCAGGTATTTGCTTTGCTTGC
WI-7992	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAACTGCTTGAATATNCCAGATTTGTTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTTCTTCACGAAAATAAATTGCTATCAAGAGCAAAC TATGAACAATTATTATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGGGCAGGTATTTGCTTTGCTTGC
WI-8004b	183	C	T	ACTAAGAGAAATTATTTATTGGTGGCCTATAAAACTCTGTTCAGTCTTTACCTTGCTAATGATTTATTTT CATTAAAGTAAATGATCATCTTTGGGGAGGCCATTTTATAAAAACATATTTAGGAGAAAATTTCTTTGA TTTATGCTATAAGGTAAATGTTGCATAATTCTTGCCTATGTGAATTG[C/T]AGGTTTCCACTTTGAG AGAAATTCTCTCAATCTAATAATAAAAGACCAAGGGCCAGAAACACTAAGATA
WI-8021c	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAAACCTTCACCACACAAGGAGTTTTCTTGTTAGTGATTCTCAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCCTTCACTTGAGATTCTTTCTTTGCGCCCTCTCATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCTTGTTAGGGTGATTCGAATTCGGTGAATTGCCA

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WI-8021b	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAAACCTTCACCACAGAGTTTTCTTGTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCACTTTGAGATTCITTTCITTTGCGCCCTCITATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCTTGTTAGGGGTGATTCGGTGAATTGCCA
WI-8021	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAAACCTTCACCACAGAGTTTTCTTGTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCACTTTGAGATTCITTTCITTTGCGCCCTCITATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCTTGTTAGGGGTGATTCGGTGAATTGCCA
WI-8024c	206	A	G	CTGAAAAATTACTATGTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGTATTCAGGAGGACAGGGCAGAGGGATCCCAGTGGCCACTTCCCATGGGAAGACAGAAGAGAGT GGGGCCCCAGAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACCATTTCAGCCGGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAAGAGC
WI-8024b	206	A	G	CTGAAAAATTACTATGTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGTATTCAGGAGGACAGGGCAGAGGGATCCCAGTGGCCACTTCCCATGGGAAGACAGAAGAGAGT GGGGCCCCAGAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACCATTTCAGCCGGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAAGAGC
WI-8077	167	A	G	GAATGAGGCCTTCCTAGCGCCGAGGGACCTGCTGCTGTTGTGGCCTGCACACGCATTCTATGGAATGC TTTTTGGCCAAGCGGGGGCCACTGAGGACTAAGCTCTGANNNNNNNNATCTCGCCCAAACTCCTTTCT AAGGAGTCTGGGGTGTCATGCCTCAATCTGACTCTGGCATAACAAGGGAAAA GTGTATTGTGACTTACTTTCCAATCTGACTCTGGCATAACAAGGGAAAA
WI-8118f	114	G	C	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACCACTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGTGGAAACTGGCAAATACAGAATTG[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A	G	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGA[A/A/G]TGACCACTCCCTTGCTAAGGAAGCTAT TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T	G	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTGTTTT[T/G]CTTAGCCTTGAAGA TGACCAGGTAGAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44	C	T	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGA(C/T)CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAAACTGGCAAATACAGAATGTAGCTTGTTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGACCAGTAGTCTTTCTGATTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88	T	C	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC(T/C)GGCAAATACAGAATGTAGCTTGTTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGACCAGTAGTCTTTCTGATTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299	C	T	---	TTTTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCTGTGAGGAAGGGCAGGTGGGGAGGAGGGCCCTCTTGGCACACA TTTATGGAGGGGTTGTCCCTGAAGAGAGGGCAGGTGGGGAGGAGGGCAGGTGGGGAGGAGGAA ACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAAACAATCACGGCA
WI-8171c	46	A	G	---	TTTTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC(A/G)TGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCAGCATTCTGTGTAGAGGAAGAGACAGGAAAGGAGACCCTCTTGGCAC ACATTTATGGAGGGGTTGTCCCTGAAGAGAGCACAATGAAGAGGATGATGATAAAAAACAATCAC GGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171a	46	A	G	---	TTTTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACAAC(A/G)TGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCAGCATTCTGTGTAGAGGAAGAGACAGGAAAGGAGACCCTCTTGGCAC ACATTTATGGAGGGGTTGTCCCTGAAGAGAGCACAATGAAGAGGATGATGATAAAAAACAATCAC GGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171b	298	T	C	---	TTTTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCAGCATTCTGTGTAGAGGAAGAGACAGGAAAGGAGACCCTCTTGGCACACA TTTATGGAGGGGTTGTCCCTGAAGAGAGGGCAGGTGGGGAGGAGGGTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAAACAATCACGGCA
WI-8314b	85	G	C	---	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTC(G/T)AAGGGGAGTCTCAAAACCCCAGCTCAAAATAACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATCTCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78	C	G	---	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCT(C/G)TAAGGGGAGTCTCAAAACCCCAGCTCAAAATAACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATCTCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

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WI-8321	178	G A	TTTTAAATATGCCCGTTTAGAGCAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTTATACTGAGTCTGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT[G/A]AGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8321	178	G A	TTTTAAATATGCCCGTTTAGAGCAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTTATACTGAGTCTGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT[G/A]AGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8332b	123	A C	TATGTACTCACTTTCAGTTACCCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGCGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAGTCTTCCCTTGCAGCCTTAGA[A/C]ACTAAGTAG CAGTACTGTTTGGTGTGTGTTGTTCTTCCCCAGCAATGCCTACTGCGAGCTACTTAGTAACAACTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C	TATGTACTCACTTTCAGTTACCCCCGTGCCTCCAGAATCGCATGTTGCTCCTGTGC[A/C]GCCTTAGAAAACTAAGTAG CAGTACTGTTTGGTGTGTGTTGTTCTTCCCCAGCAATGCCTACTGCGAGCTACTTAGTAACAACTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCACGAGGAGGAGAAAGAGAAGGGAGAAGTCTACACACTTTT AAACAACCAGATCTCATGAGANTTCCATGGGAGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCGTGGGG
WI-8378	308	T C	TGCGGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGGAGAAAGAGAAGGGAGAAGTCTACACTTTT AAACAACCAGATCTCATGAGANTTCCATGGGAGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGCCCCTCCTCCAACACGTGGGG
WI-8426	184	T G	TTTAGCACATATTTAGCATTAAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNTTAA GAGGNTTCTTTTGCTGTGGANGGGTGGCTTGCTTGAACTTCCATTCTGT[T/G]GCCTTGTAGCTGGTG AGGCTGGGAGTATGGGANGGNCCCGGGGCCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCGCCCTTCTCACATACACT[C/A]CA TCTTCTATCTTAGTTCCAAGTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAAACTATGATTTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

Name	No.			Sequence	
WI-8450g	55	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTATCTTAGTTCCAAGTTTAGTTTTCAATCCAATTATACCATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAG	...
WI-8450f	108	T	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACTACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTTCAATCCAATTA[T/A]ACCAATTCCATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAG	...
WI-8450e	125	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTTCAATCCAATTATACCATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAG	...
WI-8450d	125	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTTCAATCCAATTATACCATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAG	...
WI-8450c	108	T	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTTCAATCCAATTA[T/A]ACCAATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAG	...
WI-8450b	61	C	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTACATTTTAACAGCCCTTCTACATACACT[C/A]CA TCTTCTCTATCTTAGTTCCAAGTTTAGTTTTCAATCCAATTATACCATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAG	...
WI-8450a	55	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTAGTTTTCAATCCAATTATACCATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAG	...
WI-8458b	60	A	G	CAAGGAAAGCTGTCAGTCTTCATAAACTTCAAAGAGTTACAAAAATACGTATTTTTTAA[A/G]CTA CAATTCAAGATTAGCATCCAAAACCTACAAAACATGATTCGTCACACACCATACAACCTTCAC ACCTGGCTACAGCAGCAATGTTGACTTACATCACCATTGTTTATACTTGTGAAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCGAGTTCTCA	...

ID	Pos			Sequence
WI-8461c	105	A	T	CTTCCTCCTCCAAAATCTACACATGAATACTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAAATGATATAATATAAATCATTTTT[A/T]NNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38	T	C	CTTCCTCCTCCAAAATCTACACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAAATGATATAATATAAATCATTTTTNNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38	T	C	CTTCCTCCTCCAAAATCTACACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAAATGATATAATATAAATCATTTTTNNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105	A	T	AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAGTGACTTAATTTTGATAAAAAT TAAAAGCAT[A/G]AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAAAATATTCTTCCCTTGTCTTTTGTCTTTTAAAAAACATTATTCTGAAAAAAAAAA ATCAGAAAAAACATGATCGTGGAGAGAATTATTA
WI-9438	77	A	G	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAATCCCAGTCTGTCAGCTCAGTACCTGT[C/T]GTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACTTAGAAAAACAGCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9439b	101	C	T	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAT[C/T]CCAGTCTGTCAGCTCAGTACCTGTCGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACTTAGAAAAACAGCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9439a	76	C	T	GCCTGTAACTTAGAAAAACAGCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9446b	75	T	C	GAAGGCTTGATTAAGGGAGGNTTATTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAA[T/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTCATATGTGTTTGTNCCCTACTNTTATCACTGTGTCTTGTCTTTTGTCTCACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

Clone	Position				Sequence
WI-9446	75	T	C	---	GAAGGCTTGATTAAGGGAGGNTTATTGATGTNAACTTACCATTCCATAGAGACTATAAAGANCATTA TAAAAAA[T/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTAAAT TACTCATCTTTCATATGTGTGTTGTNCCCCTACTNTATCACTGTGTGTCTTCTGTCTTTGTCTACCTA TGNGAACTGCACACTATCTGTGTGGCAATATTGT
WI-9497b	185	A		---	ATTAAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACTTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTCTTCTTCTAGAGTGTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACATGGAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9497	185	A		---	ATTAAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTCTTCTTCTAGAGTGTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACATGGAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9523b	193	C	A	---	GTGAAAAAGTTTCTATTCCATCATCATACAATAGATTGTGCTAAG[G/A]ATCATTTTGGAAGAAT GTGCAGCATTCAGAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTCAGCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAACAACTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G	A	---	AAAAACACAAGTTTCATACATCCATTATAACACAGAAGTGATTATTACCAGAC AAGCCATCAGTGATGTATACTGCCTTNCTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCAAGAACAACACTAGAGTCCTACACCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG G[T/C]CGCTGGATACCACTAAGAAGTCTACTGCAGCCATGTTGGTATGATTT
WI-9554	202	T	C	---	CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAAATACAGGTAAGTATTCAG GGNTAAAATGGTACAAAAAAGGCTGTAACTCTTTNCTTCACATTGATCACA
WI-9555	97	G	A	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAACTTTGGAAAAAAAAAACACGCACA TAAGTATCATAAACTGAGGGTTGTGAGACAGTTAC[A/T]GTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTCATTTAAAAAACACACTGACAAATCTTTC
WI-9625b	172	A	T	---	

Marker	Position	Allele	Allele	Sequence
WI-9625	172	A	T	TTGAACACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCCATATATTTGTATCTNCTCCTTGGGAAAAAAAAAACACGCACA TAAGTATCATAACTGAGAGGGTTGTGGACAAGTTACTTCTCT[A/T]GTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTCATTTAAAAAAAACACACTGACAAATCTTTC
WI-9647	144	C	T	TTTTTCTGAGATTCAAAGAGCTACACATTTTGGTTAGTGTATGTCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTCACATTTTAGGTGATGCTGTCTCTTGTAAACAGTAGTTATTGCTAGACCTAAAAATCCAAGCT TACAACT[C/T]GTCCTTTACCTGATACATTTATTCCATTTAACTTCATTTGGATTTTTAAAAATGTTA ACTTAATACGTCTCTTTCAGATGTCCCTGCTTTTTAGTTAATTGTGTT
WI-9676n	114	A	G	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCAATAACTTGA GGCCAGGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676m	184	G	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGC[G/T]CATGAAATAACTTGA GGCCAGGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676l	84	A	C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTG[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676k	202	C	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGAGG[C/T]CAGGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676j	92	C	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTA[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676i	173	T	C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTT[T/C]CCTCTGTGCGCATGAAATAACTTGTTGTT GGCCAGGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT

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WI-9676h	134	C	A	GGGCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676g	202	C	T	GGGCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676f	184	G	T	GGGCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGC[G/T]CATGAAATAACTTGAG GGCCAGGGTCTCTCAGCT[T/C]CCCTCTGTCATTGTTTGTTT
WI-9676e	173	T	C	GGGCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGAGATGTGGCTTTCCTGCCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676d	134	C	A	GGGCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCATGAAATAACTTGA CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGCATTGTTTGTTT GGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676c	114	A	G	GGGCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676b	92	C	T	GGGCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTG[A/C][G]TTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676a	84	A	C	GGGCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA

WI-9738b	40	C	A	TGGACCAAACACAGACAGAGATGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACAACATCAACATCTCAAGGAGTCCATTGTTCAAAAACAGTAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCCTGGGGCACATGTCTGTATTGCTGTCC TCTTTTTATTTCTGTCCCTTATGTTGGTGGGCACATGTCTGTATTGCTGTCC
WI-9738	40	C	A	TGGACCAAACACAGACAGAGATGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACAACATCAACATCTCAAGGAGTCCATTTGTTCAAAAACAGTAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCCTGGGGCACATGTCTGTATTGCTGTCC TCTTTTTATTTCTGTCCCTTATGTTGGTGGGCACATGTCTGTATTGCTGTCC
WI-9756	47	A		ACTGAAAATGTAAATGGCCAAGGCACCCAGGACCTTAAAAAATCATAAGAAGTTAATCTGTGGGAAAA GAGTAACTACAAAAGCATCTAAACAAGAGCAGGATGTAATGTGTCCCCTTATCACTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACAGAATATACACTTTTGGAAG ATTTCCACTTAACCACTTGATTCTTCACTTTTTATGATTTAAAAACTCTCCGTGG
WI-9758	135	A	G	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGAGAATTCAATTCAAAGAAGAATTCTTGTTCGCAAGGTCAATTTTTATACTATTTA A[A/G]TAAAATAAACTCTGGTAGGTTCTATAGCAAATGCTAAGTAAAGTAACCGCTGGTTCTCAAATT ATTACG
WI-9778	127	G	A	ATTTAAATCGCAGGCAGCGGGGGGAAAATGGATACTTTCATATGTCTCTGTACCCAACTATAAACTTTG GTTCTCATGCCACCATTTCATTTGCCTTCCACTCCAAGTACCACTGATTTTACCAATT[G/A]CTCTC ATAATTGACTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTCTCTATTACACACTTGCCTCA AAGAATGTGTCAGTCAGTTCAGGACTAAAGGCAATAGTCTCAGGGCAGCAGCC
WI-9832	116	C	A	TCTCCCCTTTGCCTCCTCATGCCCCACTCCCTGCCACAGAGGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAATGCAGTTTC[C/A]TGGATCCCACCCAGGA CTCAAAAAAACTAGGAATTGGGAAGAGAGAGGGACCTGGAATCGGTGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGGACCCAGAGCATGGAAGGTTGGCTTGGC
WI-9841	101	A	G	TGGAAAAATAGCTTTTATCAATCTCTGATATCTCTGATATGCTCACATGTCTACATATGTAGGAGAAATGCAGAAATGGCATGA TATGAAATTCCATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATACTTATTAACACTT AGGATTATATACACACAATAAAACGTCTGTAAGGATAAAACTAAGGTTCTATCAGTGGGAAATGAGA TTTGAAAAGAGGGGATGTGTTACTTGATATGCTGTTG
WI-9880c	222	G	A	GAACTAACACCTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGTGGGGGTTGAGTTTTTATGATATCTCCTGTTAGACCCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAAATTATATTTTATATAAGCACATGAA AATGGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACACATATTTG

ID	Pos			Sequence
WI-9880b	157	C	A	GAACTAACACCTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGGGGTTGAGTTTTTTATGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACACATCCTTGGA[C/A]TATATAAGATCCTCTTTAAAATTATATTTATATATAAGCACAT GAAAATGGAATGAAATAAGAGTTGACATAGGAATTACCTACACATATTTG
WI-9880a	108	C	T	GAACTAACACCTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGGGGTTGAGTTTTTTATGATATCT[C/T]CTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAAATTATATTTATATATAAGCACAT GAAAATGGAATGAAATAAGAGTTGACATAGGAATTACCTACACATATTTG
WI-10183	127	C	T	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACTTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTCTGCTGGAGTTTATTTTAAAAAAACCAGCCCCCAGTTATCACAGTTTCTNTTTTTGT[C/T]CACC ATTTTCCATAACAAAAGAAGCTACACAAAATTNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A	G	TCCCTCAATGACAGATGAACTAAATTTCTCTTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A	G	TCCCTCAATGACAGATGAACTAAATTTCTCTTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C	A	ACAACGCTGAACTTCCATAACAGTCAATGGTACAGTCAAACATCACATGTACAGAACACACAATTTA GATGAACTGAAATTATAAGNTAAATAAAAAAT[C/A]CAATTTCAGNAAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATTCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACACATGACCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C	T	CGTTCCTTTCCTTTTGAGATTGCAATTAAGTAAGTAGAATAATATGAGAGAGAACTGACAATTGGGTTGTCC TACTGAGCTTGGGCGCCAGGTGTGTACTTAGGAACCCAATCCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTC[C/T]TGACCACATACATGCGGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTCC
S72904	51	G	T	AGCATAGAAAGTGATTTATATTTTAATGGTTTCAAGTGGAAGTTCCTT[G/T]AATTTGTCAGTTC ATTCCTGGAAAATCTTTTGAGTTAAAAATAAGGATCCTGAACTACAGCACCTGAACTACAGGCCCTAAA GAGAAATTGCCTCAAACCACACAAGTGCTAAACAGTATTTGGAGTGTGTTTTCAGTGTCTGTA TTGCAAAAGTCCTGATGCTAAACAGTATTTGGAGTGTGTTTTCAGTGTCTGTA

UTR-00481	115	C T	TATTCTTTTATCCTGGGGGCCACAGTTCTTGATTATTCCTCTTGTGGTTAAAGACTGAATTTGTAAACCCATTCAGATAAATGGCAGTACTTTAGGACAACACACAAACACACACAGA[C/T]ACACCTTTTGATATGTAAGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTCAGATTGAGC
ESTC1	33		CCCTGTAGCAGTCTTCAGCCTCCTCTACCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37		GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21		GCCCATCAAAATTTCCTTCACANTCAATACTGTTGAACAACAGATAACACATCTTCTTGCTCATCCCACTTGAA
ESTC107	20		TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35		AAAACCAGGAAGGCCCTGCCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23		AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37		AAGGGGACACAGTGTTGCTGACAAGGTGACACTGAACANAACAGTTTTCCTTTAATTGTAAAAGGGGGCATCG
ESTC117	24		AATTGGCTCTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAAGCCTCCA
ESTC119	24		TGTCAAGGCAGATCTTGAGGGGTTATNGTTAAGCCTGATAACAGCCTCTT
ESTC122	34		GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATGAGAAAAATCTGAAA
ESTC123	21		GAAGCCAGTATGTTGTGGCAANATTCGAGAAAACACACTGAAAA
ESTC128	42		GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAATGTGGAACTGG
ESTC129	20		AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46		GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGGTCTGGATCAGAAAA
ESTC130	49		GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAATCTACACCTGAATG

ESTC132	30	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	CCAGTTGGCTTCTGTCCTCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	AGGAGCACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGNGGGGCTGGGTCCCTGAGCTAGGAGGGAGG
ESTC14	20	---	CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTTAGAAAGCTTGCCCTGGTG
ESTC142	72	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGAGCGTAATAATCTATTTTATTCATTTTAAATCAAAGANACCATTCCATTTCCTAACAAACA
ESTC143	29	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAAITTTGTGATTTCCTTTG
ESTC144	26	---	AAATCCATATTTTCTTGACATGAGGTNGCTTTTAGCAGCATTTCGG
ESTC146	20	---	CATGTCCAGGATAAGGAGCANACCAGGATTTATACGGTGGCAGCG
ESTC148	42	---	TCTTTGGTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATGCAGCGGCCTGTGGAGGCCCCTGGGGGTGGCTGGGCCTGTGTCCTGAG
ESTC149	28	---	TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	CCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATATCAATATTAAACCTGATGTTTAAAGAAACCTAATGAGA
ESTC151	49	---	GAAGCTAAGGCCCCATTTTTTTTCTTTAATACAAAATCTACTGGTGCTNAAAACTCAGAGCTTAGGAAACACAGCC
ESTC155	37	---	TTTTTAATTGACAACTCAATCTCTACATACACATACAGTNTTGCACGAATTATAAGTGGATCAACAATTATATTATTGATACAAACTCATGAGCATTTACA
ESTC156	32	---	GCAGCATTTGTGACAGGAGCGCAAAACAAANCCTGGCTGCCTCGGGATGGAGCGGGGCGGGCCTCACCACCACTGCAT
ESTC158	35	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGCAA
ESTC159	31	---	AGCTGGCAAGAGAGACTTCCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCAGCTTTGAAAGG

ESTC16	23	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	---	TTCTAGCATTGCTGGTGCAGTGGGGGGGCCTGAGCTGGGGNGCAGTGGGCAGTGTCACTGGGGCCCGTTTG GGACTGGGTTGA
ESTC162	36	---	CTCTTCGTCCGTTTGCAAGTTGCTGTTGTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	TCATTCTCCATAGAATATATTGGTTTTGTAACANCGAATACAATCCAATATATAACATTAAAAACAATCC GATACATACCA
ESTC169	22	---	GTCTCTGGTGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAAGGTGCCGCCGTCTGTTTCCATGACTT
ESTC176	23	---	CACCTCCTCCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCTTTATTCTATTAAAATACCTTTTAT TCTCTTTATTCCCATAAAAAGGCAACCAA
ESTC18	29	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGCGCCCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	TAGGGATTCCAAGTTGCCTGGNTTTAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	GCTTGACTAGCGAGGCTACATCACAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	TCTATTAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACTCACTTGTCTTCCAT CTTGC
ESTC189	27	---	AAAGTACAAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	TCCTCAAATACCACTTTCCCCTAACTTATCAGTCTAGTAAGCNTTTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	ATCTCCAGTGTCTGCTGCCTCCTCCCNGCAAAGTCTCCCACAAGCACA
ESTC20	33	---	AAGATTAGGACAGACCGCCGGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44		TTTGGTGAAAATCCCAATATATGAGTTTAAAAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTGCCTGCAACAG

ESTC201	35	TCTTACTTGGGTAGTTTAGCAAACACATTTTTAAAANCCACATCCAACAGATTGGTT
ESTC202	22	CTGCTGGGAGGGAGGACAGAGACGGGNCAGGCGGCCTGGGTGGCGGCCCCAGAAAGGCTGGCGTGGCGGATGTT CGAGATGAGCC
ESTC203	27	ACACTTAACAGGTTAAAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAATTTATTTGTGCTAC AAGACACGTTGCA
ESTC208	43	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAAANAGCAATAACTATTGTTTAAAAGC CTAAGAGTGAAAA
ESTC210	29	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	GGGTAACCTGATGAGGAAGCTCTAGTGTGNAGAAATTCAGGACGCGGGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	CTCCAGAGTCCCTCCTCCTCANACCAGGGCAGGAGGGAGTTAGGGAAT
ESTC216	49	TGGCAAGAAATTTATTTACACTAACAACAAATTAAATTAATCACAGGTATTNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	TTTTGTCAGTAAATGAGCAATACACTGANTCGCATGATTAAATAACATTAACAAGTTCAT AAACACACCCCA
ESTC219	32	GTACACATCCTGGGGGTGAGCACACAGCAAAANGGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	TCATTGAAGAAAATTATGGGTTTATTCTTATTTCTAATTGNGAGAATGCTTAATGTGTCACAGGCTACA TAAGGGCC
ESTC223	27	CTTCTGAAGCCCAAGAGAGAGGGGCAGAANGTAGTTCTTGATTTAAAAAAACAGAAAGGGGAGGGAGGA
ESTC224	37	CGAAAGGTAGATTTCCCTCACATATTACAAAATACACANAAACACACACACACACA
ESTC225	20	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCCATATAGAAAGAGCATAAGTGCTTCAGAAGGA ATGTGTAGGATCG
ESTC23	27	TTCTACTTTATTTCATATTCCCACCACNATAACGACTCCTTTAATTTAAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	GCTTCCTCCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAATTAAGA
ESTC231	24	CAAAAGGGTTAGTTCATATTCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	::	GAAGAGCTGGGCACGCATCTGACNTTTCTTCCTCTATTCCTATAAAATAAAAGGAAGCAGAAATCT GC
ESTC3	20	::	CAGACATGACCTACCGTCCCNGGCCCTCAATTCATATTTATTCTTGAGCCGCCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	::	ACAGCCCCACAGAACTATTGTAAAACAATATTNTCAGTCGGTGATCATTGTAATATACAATACAAAG CAATTCCTCAGA
ESTC33	25	::	AGCACTTCCAGCTCCTTGACGTTGTNGGACCAGGGAACTTCCGGAA
ESTC39	26	::	AAGGAAAGGGAACCCACCTGGGCTTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	::	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAAGAAACCATT
ESTC40	22	::	GGCATGCTAGACAGAGAGGCATTANTTTTGAAGATCTTTAAAAATATTTGACTTGTTCCCCCTTCAC
ESTC45	37	::	TTTGGAGGTTTGTGTCTGGAGTTTTGTTCTTTGTAACNCTCTCATCATCGAGGCTATATATTAA
ESTC50	56	::	CTGTCCGTGGTGAGCCCTGCGCGCTGTCCCATGGGCCCAGGGAGCCACTGGTGCGGGANCCGGGCAGATG TTTACCCTGT
ESTC56	45	::	GTGCCCTGAAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGGAGGGAAAGGACACCA AGT
ESTC57	20	::	AAGTGGGCCCTCCCAGTCCCNTCTCGGGCACAGATCCCACCAGTCTGCTC
ESTC59	38	::	GAAAACACAAAAGTGTTGAGAAAAAACTTCTCAAAATTNGTTCCAGACTTCAGGAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	::	TCTGCAGCACTTCACTACCAAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATG TGGACTGAACCG
ESTC61	57	::	AGTGATTTTGGCTCTAGGCGTGGTTCTCATCTGTGAAATTCCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	::	ACAGACACAGCAGCATCACCACCANAGGGCCCACGGGAGGGTCGGGGAGACGACACTTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	::	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTTACTGCTCATCCGT CACTTTCGGCTAA
ESTC7	45	::	AGTTTCCCTAGAGCTGTTGCGGCCAGATAGCTGTTCCTGAGTTGCANGCACGCGATTGGAGATTTGGACACT G

ESTC72	37	---	GGGCCTTCCAAAATGGGTATTGGGGCCAGGAGGAGGCTGGGCNTTTGGCGTGACGCCTAAAAGTGTGACC AACAATTCACAGCTACAGAGAAATCTAGAACAAAATCAAATATTCATCACNTTGGGTTGAAAAGTTG
ESTC74	49	---	GAAGA
ESTC77	40	---	ATGACTTTCCTGTCCCATCGGAAACCAGAGTTTCCCCAGGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCAGAGAGGGCAGCACTCCAG
ESTC82	25	---	TTTCAGATGATGGGGTCTGAGATGTNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACACATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC85	28	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGGTTGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC89	22	---	ATTGCAAAGGAAGTGGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33	---	CTGGTTCTTCGTCTTGGCATTCGTCCTCCTCNGGCCAGTGCTCCACCCAAGTGTCCTTCCCGATGAT
ESTC93	29	---	CTCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTCAGGGCAGGATCC
ESTC95	32	---	GCACGTTCTTTGTTCTCCTCTTCCAGAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCG
DWU-100	127 C T	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCCTTGACTGTTCTCCA[C/T]GCCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAAGAAGAAAGAAGAAAGAGAAGGCTTAGCTG
DWU-177	77 A G	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAAGAGACGCTTGTGCTGAA TGTTCATGGC[A/G]GCCCTATTCAGCACCAATCATCGCCAAATCATGCCCAGCTTCGTCATATGAATGAGATATACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACACAACATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-286	213 A C	---	CAAATACCTGGACTATCAACCTTGTTGCTTAATCCCTGCAGCATTCAAGGTTAATCCATCTAAGTGAC ATTTTGAAATTCCAGCGGTGCCACCCAATCATGCCCAGCTTCGTCATATGAATGAGATATACATTT ATGTCTGACCTTCCCTCAAGACTGATTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[A/C]TGGGAAACCAGCCCTATCTGAGTCTTCGGCTCCCTCC

Name	Pos				Sequence
DWU-252	94	A	G	:::	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGTGT CAGAAGGAGAGCTACAAAACCTACCCTCA[A/G]TGAGCAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGAATTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85	C	T	:::	GAACATTCCTCTGCGAGCCACTTCACTACCAAATGAGCATTAGCTACTTTCAGAATTGAAGGAGAAAA TGCATTATGTGGACTGAA[C/T]CGACTTTTCTAAAGCTCTGAACACAAAGCTTTCTTTCCTTTTGCAA CAAGACAAAGCAAAGCCACATTTGCATTAGACACAGATGACGGGCTGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTTGATTGAGAGAAATTTTACTGACAGAAAATGCAATCTCCCT
DWU-370	231	A	G	:::	GAAAATGTTAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAAGAG AAGCAGCATCATTCCCCAACAGGGCAACTGTAGAAGGCCAGCTGAGAAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCCT[A/G]GCATCTATTTCCTCTGTGC.
DWU-1537b	89	A	G	:::	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCACATAGCTCAGGTAATC CAGGAGCCAGAAACCCAGGAGC[A/G]TGGGACCTGATCCACAGTCAGTGGGGGACTCTGTAGCT ACAGCATTTTCCTGAACACACAAGAAATCCAGTAAGCAGCACACTGGCTGA
DWU-1537a	52	C	T	:::	CTCTTAACTTCAGTTCCCTCTATCTATAAGAATAAGGGATTCAGTTGTGATCA[C/T]ATAGCTCAGGTA ATCCAGGAGCCAGAAACCCAGGAGCATGGGACCTGATCCACAGTCAGTGGGGGACTCTGTAGCT ACAGCATTTTCCTGAACACACAAGAAATCCAGTAAGCAGCACACTGGCTGA
ESTD-ADAb	196	C	G	:::	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGAGCCCTCTCTCCCTGGGATTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCCTGGGAATTCCAGGGTCACTGTTCCTTCCTGTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCGAGAAGTGGGACTGTGAGGACATGGAGGGCCTCG[G/A]ACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTCCTC
ESTD-ADAa	184	G	A	:::	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGAGCCCTCTCTCCCTGGGATTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCCTGGGAATTCCAGGGTCACTGTTCCTTCCTGTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCGAGAAGTGGGACTGTGAGGACATGGAGGGCCTC[G/A]GCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTCCTC
ESTD-ANT1	160	T	C	:::	TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTGGGAAACAAGAAAGGGGCCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTTATGGAGGACCGAACTGAGGC[T/C]GAGCTCAGATGATCCTGT
EST10398 2b	168	A	G	:::	TGCCTGGGGTGGCAAGGCTGCCAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCCTTATCTCACTGACGATGTTCACATTTGGGGCTGACTTTCCAACACGGAGAAG CATTGTTTTCTTCGGGCCAAGAAGGTATCTACCC[A/G]TATAGTGTCTATTAGGCATTTG

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EST10398 2a	147	C	T	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGCAACCCAGGAGGCTTTATGAAGAGGCGGGCCATGGTAAGATGCTGCCACCTCTTATCTACTTGATGATGTTCACATTGGGGCTTGACTTCCAACACGGAGGAAGCATTGTTTCTT[C/T]GGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14	G	C	ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-D4S95	90	T	C	CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTTGAGAAGAGCAAAACAACTTTCAAGGATAATGGGCAATCACTTTCTTT[T/C]CTTCTTTAGAGTCTACCGG
ESTD-GPPK2L	38	G	A	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACC[G/A]CCGAGAACTGCTCGATATC
ESTD-HRASb	82	A	G	CTGGGCTCGCCCCGGCCAGCTGCTGGCCACCTGGACGGCGCCGCCCAGGCCTCTATAGTGGGGTCGTATTCGTCCACAAA[A/G]TGCATCTGGATCAGCT
ESTD-HRASa	37	C	T	CTGGGCTCGCCCCGGCCAGCAGCTGCTGGCCACCTGGACGGC[C/T]GGCCGCCCAGGCCTCCACCTCTATAGTGGGGTCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-NRAMP	81	A	G	GGAGGCAGGAGGTGGGGAGGGGGTCTGTCTGCTCCCAGGTCCCACAGACCAGAGAAGCGGCCTCAGTGTATCCCCCACCCCA[A/G]TGTGGGCGCTGGGAGGATGAAGGAGGAGTTGATGCAGGT
ESTD-OTC	18	A	G	GTGACCTTCTCACTTTAA[A/G]AAACTTTACCGGAGAAGAAATTAAATATATGCTATCAGCAGATCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
EST36751 7	36	C	T	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTTAACT[C/T]GATTACTTTTCTATTCAAATCTCTGTAAAATTGAAATATGAAACTTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109	A	G	CACGTGGAAAGGAGCTATTTTTGGAGAGGCTTTAAGAGTAAAGAAATCTGTCCCCAAACTTGTGGCTGACTTTATGGCTAAGAAGTTTTCACTGGATGCATTAATAACAAAAT[A/G]TTTTACCTTTTGAAAAAATAAATGAAAGGATTTGACCTGCTCGCTCTGGAAAGAGTATCCGTACCGTCCTGACGTTTTGAAACAATACAGATGCCTTCCCTTGTAGCAGTTTCAGCCTCCTCTCTACCCTA
EST18288 3	121	C	T	GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAAGATTGACAGGTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCTGA[C/T]GGGGAGCCAGTGTGGACAGCAGCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTCTGCTGGCTCTGGCCCCTAGGGACTTAGTATCC
ESTD-AK-168	31	C	T	GGGAGTGACAGCTAGAGCACCAAGGGGGGGCTC[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTCATTCTGG
ESTD-ALB	180	A	G	AATCCCAGCACTTTAGGAGGCTGAGGCAGGCAGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGCATGCCTGTAATCCCAGCAGGCTTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAGCCGAGATGGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTTC

EST705233	182	G T	---	TTCCCGCCCAGCCCCCATCCTTGGCCACCCTGGTCCCCCTCAGGGGCCCACCCGCGGCCACTCACGCGCTCT CGGCTCTCCGGTAACATCCGGCCGGGGCCGCCGGTCCTTGAGCACACATAGCCTGGACCGTTCCGTATAGGAGG ACCGTGTAGCCGTTCCTTCCTGTCCCGGCCCTTGCCAGGGGCCAGCCCT[G/T]CAGAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGGAGTGTCTCCCACGTG
ESTD-APOA2	101	C T	---	CCAGGTGTTGTGGCCACGTGCCTGTAATCCCAGCTACTCGGGAGACTACTGAGGCATGAGAATCTTTGAAC CGGGGAGGCGGGAGGTTGCAGTGAGCTGACATCG[C/T]GCCACTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
EST587077	112	C T	---	CAGTGTATCTGGAAAGCCTACAGGAGCACCAAAATAAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCACATCTTTGGCTCACATGAAGGCCAAATTCCGAGAGAC[C/T]CTAGAAGATACACGAGAC CGAATGTATCAAATGGACATTCAACAGCAGGAACTTCAACATACCTGTCTCTGGTAGGCCAGGTTTATA GCACACTTGTCACCTACACATTTCTGATTGGTGGACTCTTGCTCTGCTAAGAACCTT
EST741676	137	C	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAAATCTGGAGGAACAACTGACCCGGTGGCGGAGG AGACGCGGCGACGGCGTGTCCAAGGAGAGCTGCAGGCGGCGGCGCAGCCCCGGCTGGGCGGCCGGACATGGAGGA CGTGCGCGGCGGCCGGCCTGGTCAGTACCGCGGGGCGAGGTGACCGCGGCCATGCTCGGCGGCCACCGAGCAGCGAGGAGC TGCGGGGTGCGCCTCGCCTCGCCACCTGCGTAAGCTGCGTAAGCGGCTCTC
EST432118	132	C	---	CGCCTGGTCGCAGTACCGCGGGGCGGAGGTCGCAGGCCATGCTCGGCGGCCGAGGTCGCGGGTGCG CCTCGCCTCCCACCTGCGCACCTGCGTAAGCGGCTCTCCCGGTAAGCGGCTGCGATGGCCTGCGAGAAGCGGCC TGGCAGTGTACCAGGCGGCGGCCCGGGGAGGTACCGGGGCGAGGTGAGCGCCGGCCATCCCGGCGGCCGCCCTG GGGCCCCTGGTGGAAACAGGGCCGCGGCCGCCGTGTGGGCTC
ESTD-ARSB	126	A	---	GGAAGAAAATGGAGCCTGTGTGGGAAGGAGGCGTCCGAGGGGTGGCTTTGTGGCAAGCCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACCATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGCACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCCCATCCCCCAGAATTGAGCTGCTGCATAAATATTGACCCAAAC
EST367704	144	A	---	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACACCAATAATACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCCGATAGGGCCTGGGCCTGACCAAAAATATACTGGGTTTCCTGTTTCCTTTTCTGATCAT TCTTACAAGTTATATCTTATTGGAAGGCCCTAAAGAAGAGGCTTATG
EST260211	137	A	---	TAATGTAAGCTCATCCACCAAGAAGAAGCCTGCACCATGTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATAATTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAATTGAAAGGAGAAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTCTTTCCTTTTGCAACAAGACAAAGCAAAGCC
ESTD-BA511	29	A G	---	GGGCAACATAGTGAAACCCCATCTCTACA[A/G]AAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTGTAGTCCCAGCTACTTGGGAGGCTGAGGTCGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCCAAGATGGTGCCACTGCA

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ESTD-BCL2	116	A	G	AGCTGGATTATAACTCCTCTCTTCTTCTCTGGGGGCGGTGGGGGTGGGGAGCTGGGGCGGGAGAGGGTGCCGTT GGCCCCGGTGCTTGCTTTCTTCCTCTGGGAAGGATGGCGGCCACGCTGGGAGAAC[A/G]GGGTACGACAACCGGG AGATAGTGGAGTAGTACATCCATTATAAGCTGTGTCGCAGAGGGCTACGAGTGGGATGCGGGAGATGT GGGCGGCCCGCCACCGGGCGCCCCCGCCCCCGCACCGGGCATCTTCCTCCCA
ESTD-BCR	69	C	T	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGACCCGGAGACTCATCATCTGCGCAAGA GA[C/T]CAAAGAGGTCAGCTTCTGTTGTCCCGGGAAAGGGAGGCAGGTGACAAGCTAACTCTGCTTC AAAATCAACCATCCGGTGGACACTGTGTGGCCTCGCCATCTGCCTGCACA
ESTD-BRCA1aa	119	C	T	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAAGATCTCATGTTAA GTGGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA[C/T]GGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACA GAACCAAATAAAT
ESTD-BRCA1bb	139	A	G	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAG[A/G]AGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAATGAAA
ESTD-BRCA1cc	126	A	G	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATAAAGGAAGATAC TAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGA[A/G]AGGA GAGCTTAGCAGGAGTCCTAGCCCTTTCACCCATACACATTGGCTCAGGGTTACCGAAGAGAGGGCCA AGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST512120	122	A	C	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTGTGCTCCCCACTCAATACA[A/C]AAAGGCCCCT CTCTACATCT
ESTD-C1R	40	A	G	ACACAGGTGCTGGCCACTGGGGCTGGGGATCCTCTCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCAT CAA
ESTD-C1R	40	A	G	ACACAGGTGCTGGCCACTGGGGCTGGGGATCCTCTCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCAT CAA
ESTD-C6	31	A	C	CCCAGTCAGTTGGGGGACAGCCATGCACTG[A/C]GCCTCTGGTAGCCTTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST201182	119	C		GTTCCGAATCCTCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGGCGGGCTGTGGTCCAGCT GAGGTGAGGGGCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGGTCTTGCTGCTGTCCATCCTAAGCT CTGAGA
EST530186	67	A	G	ACAATCCAGGTCACACATTCCAGGAAGGAAGGAGGCCACGAGGATCGAGGTTAGTGAAGTC [A/G]GGGATTCAGGAAGGAGGAGGCCACGAGGATCGAGGTTAGTGAAGTC

ESTD-CB22	119	C T	GGCAAGTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAGTGCCAGTGCCAACCCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGGTAGAAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCCTTCTCTCTCACACAC
ESTD-CB23	136	C	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTCTCTCTCACACATACAGAGAGCCTACCAGGACCAGAGACAGCT CTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTTCCCACCCGA GGTCGCTGTGTTTGAGCCATCAGAAGCAGGAGATCTCCCACACCCAAA
ESTD-CB24	145	A	ACCAGGACCAGAGACAGCTCTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCCGAGGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCGACCACGTGGAGCTGAGCTGGGTGAATGG GAAGGAGGTGCACAGTGGGTCAGCAGACCCGCAGCCCCTCAAGGAG
ESTD-CB25	146	A G	GTTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTTCTCTTTTTCTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCAGGGCATGAGAATCCACGGGGCGTGAGGGAGGCCAGCGGCCACCTG TGCACAGGT[A/G]CCTACACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGGGCTCTAACCAATAAAAAAT ACCATCTCTATGAGATCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	125	C T	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGGCTGGTTGCATTTCAGGAGTTGTCTGTGGAGTTCTGCTCATCACTGAC[C/T]TATCTTC TGATTTAGGGAGGAAAGCAGCATTCCCCTTGGACATCTGAAGTGACAGCCCTCCTTTCTCTCCACCCAATGCT GCTTTCTCCTGTTCATCCTGATGGAAGTCCTCAAAACACCATTTCCATACC
ESTD-D4S338	59	A T	TTTTCTGTTTCCCTGTTGTTCAGATCCTTCAGAGAGGAATCCCTATATATGGCAGGTATATGA[A/T]ATGTA TTTCTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAATGTTA TTTTAGCTGTCGAGAAAACAATACTAATCTTGCATATGTTCATCAGAGCCCCTTGGGTGACCAGGGTGTA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD-CYP2D6	61	A G	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGACGAGAACAGGTCAGCCACCACTATGC[A/G]CA GGTTCTCATCATTGAAGCTGCTCTCAGGGTTCCCCTTGGCCTGGCAGGGGCCGAGAGCATACTCGG
ESTD-D11S1873	40	A C	AAAAAAACATTTAACACCTTTCAATCATCATATACACCATA[A/C]ATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCATAAACTGATTAATGCAACAGTTCAACAG ACAACTTTCCCAAGCATCTACGCATCAGAAAGGTCAAAATTATTACACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD-D17S33b	169	C T	CATCCCCAAGCCCATCCTCTTAGCCACCTGGCCATTTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCGCCCTACCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGGTG GGGGTTGTGTGGGGCTATGTGGTGCTTTGTGTTCTTTCCACCTGAGCGAGCCTC ATTGCAGATTGCTTTGTCTTTGTCTTCCACCTGAGCGAGCCTC

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ESTD-D17S33a	75	C	T	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCTCTGACAGAGATACACTCAGGGCCGT CATGCTGC[C/T]ACACATCCAGGGGCGCCCTACCCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGCG GTGGGGTTGTGTGGCTATGTGGTGGTCTATGGTGTGTAGACGGGGCGTTTGGTTCAGTTGCACTATTGCGTT ATTGCAGATTGCTTTGTGTCTTCTTCCACCTGAGCGAGCCTC
ESTD-D18S8	133	A	G	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGCGGAGGAATTGCTTGAACC[A /G]GGGAGGCAGAGCTTGCAGTGAGCCAAGATGAGCCACTACAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD-D3S11	44	A	G	AACTGATTAGAACCTGAAAATACATATTTATCTGAAAAAAGTGCGAGTTATTGGCTCATCACATTGG AATTTTTGCATCATTAAAAAAATCCAATAAAGTACACTGTAATAAAGAATTTAACAGAATATCATTGT TTATTCAAACTATTTATCCACTTATTTATTGGTAAGCCATACTAAATTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	37	A	G	AGGTTCCACATTATTGCTGTGATGTTTGCTGATGTTTCC[A/G]GGAGCCTTGATGTCATTCTGTATCCT CAGGTATCCCACCTTGAGACGTACTTTTCAAAAACTCTCTACAGCCGGTTGTGTTATTAATTCAAGGT TGAACATAAAGTA
ESTD-D3S2b	247	C	T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC TGAGTCTTATTCAAAACTGACAGCGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGAGTGTCGTTCGGTCTTCACGATGG CAGGTATGAAATAATATAATCGTCCTTATTGTTATTGGAAGGATGC[C/T]GGT
ESTD-D3S2a	248	G		GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC TGAGTCTTATTCAAAACTGACAGCGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGAGTGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATCGTCCTTTATTGGAAGGATGCCGGTATGT
ESTD-D7S399	83	A	G	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCTGAATCTGCATCTAGCCACCTCCATAGAT AACTGCTAGAGACCC[A/G]GTCTCCTACATCCTTTCACAAACATTTCATCCCATGGACTCCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146	A	C	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCTTGCACGTGTCGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCCTGGGGCCTCACTGTCCCTGGGGAGGAGGGGAGTGGGGGGGGAGGAGGACA GAATGCTGATT[A/C]TCTGGTGGAGAAGGGGGAGCAGCAGCTGTTGGGGGCAGCTGCTTCCAAG ACCTCCTGATTTGAGGAAGGGAGGCAGCAGCGAAGAGCGAAGAGAACAGAGT
ESTD-DMa	66	C	G	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCTTGCACGTGTCGCTCAAGCAGCTGCTCGGCCTCCA[C/ G]TCCATGGGTGTGGGGCCTGGGGCCTCACTGTCCCTGGGGAGGAGGGGAGTGGGGGGGGAGGAGGAGA CAGAATGCTGATTATCTGGTGGAGAAGGGGGAGCAGCAGCTGTTGGGGGCAGCTGCTTCCAAGA CCTCCTGATTTGAGGAAGGGAGGCAGCAGCGAAGAGCGAAGAGAACAGAGT

				Sequence
ESTD-DRD1	154	C	T	TCCCCAGCCTATCGGTCATCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCAACCTGAACCTCGCCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGC[C/T]TCGCTATTAAGAAACTAAGGTAC
ESTD-DRD2	144	C	---	TCTGCCTTTGGTGCGCAGGAGGCTGCCGGCGGAGCCGAGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCACCCCGAGAGAGGACCCGGTACAGCCCCATCCACCCAGCCACCAGCTGACTCTCCCCGACCCCG TCCCACCACGGTCTCCACAGCACTCCCGACAGCCCGCCAAACCAGAGAGAAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCCAATG
ESTD-DRD3	109	C	T	AAGAGGATGGCCAGGATGAGCGGCGCAGTAGGAGGGCATAGTAGGCATGTGGGCGGCGGCCTGGCTGG CACCTGTGGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGC[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGAGGAGA
ESTD-ERBB2	93	C	T	TCTTTCAGGGATCCGCCATCTGCGCCCTGGTTGGGCGCCTGGTTGGGCCATCGCTCCGCTAGGTGTCAGCGGGCTCCACCAGCTGG GGTGAGGGGGGTGGTGGGTCAGTGC[C/T]GGGGGCGGCCGGTGCGAGACCCCACGCGGGGGCTGGGAGGGGACTTCA CCCCCGCCCTCACCTCCGTTTCCTGCCAGCGTCCGCATCGTGTACT
ESTD-ETS2	43	A	G	ACTCACAGTGCTCTTTAAGTGAAAATGGTGAGAAAGAGAGGCACC[A/G]GGAAAGCCGTCCTGGCGCCTG GCAGTCCGTGGGACGGGATGGTTCTGGCGTGTTGCCTTTGCAACCAGGAACAGCAGCGAGCATGTCGTGGGACACA CACAGACTATTTTAGATTTCTTTTGCCTTTTGCAACCAGGAACAACCATGTCATTTCAGAAGAGTTAGTTTG AGGGTAGGAGGGGTGGGAAGGAAACAACCATGTCATTTCAGAAGAAGTTAGTTTG
ESTD-F9	111	A	G	AGATCCTGATGATTTTTTCCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAAGTATGATGTTTA[A/G]GTCAAACTTCATTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAATTTGTAAAACAAAAAC
EST687875	144	A	---	CTTCCTATGGGATTTGACTTTATTTCTTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTTGAAGCTGACAATTACACAGAAGGAAATAAAATTCACAGTCAA AGAATCAAGCACTTTCTGAAACATTGAAGTTGTTTTGAAACTTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
ESTD-GCDH	200	C	G	CGCAGACCGGTCAGTGTGGGGGTCGGGGAGTGTGGAGGGAGGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGCTGCAGAGAAGAAAGGCGGGAGAACACAGAGGCCAACTGGCTAA GTGTAAGGGACCTCTGGTCGCACCGTGTTCTGCTGCCCCTGTTCAGCTGTCGTGCGCGGAGT[C/ G]GACTCTGTCCCGGAAATTCCGAGAGCT
ESTD-GCK	88	A	G	GTTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCCACTCCTGGTCCACCATGAC AACCACAGCCCCTCTCAGGA[A/G]CACAGTAAGCCCTGGCAGGAAGAATCCCCACCCACCTGGC TGGAGCAGGAAATGCCGAGCGGCGCCTGAGCCCCAGGACTGGGAGAAGCAGCGGCTAGGAGGATGTGAGAGACAGTC ACCTGCAGCCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG

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EST34088 2	62	A T	GTGGGGGCAACAGTGGGAGAGAAGGGGCCCACAAAGAGACCGGCTC[A/T]AGGATCCCAAGGAGGCCCAACCACTCAGGGTATAAAAGGGGCGGCCAGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACAGGTAAG
ESTD-GNAT2	56	A G	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC[A/G]GGCATCATTGAAACCAAGTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154	G	GGGCTAAAATTTCCGAGCAACTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGGCAGGGAGGAGAAGATGTGTTACAGTTTGTCAGAGAGAATAAAAGGATAACCTGGGGTTTTCTGTGCTTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTTCAAAGAACGGTATACAGGGACAGCAAAGCGCAGTCGTGAAGTTTTCAAACAAGACACACCTT
ESTD-HT5	149	C	AACACACAAGCCCCAGCGAGAATTGAACCTGCGACCCCTGGTTACAAGACCAGTAGTCGCTCTAACCCCTGAGCTATGGAGCCCCTGCTGTCGTGGTTTTCTTCCTTCATCTTATAGATTGATGTTTATGCTCCTAGCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAAATTCCAGGATATTCTCCTACACAAAATGAAAACATTTTTCGTGCTCTGTAAATCCCTCGAAAAGGTTCT
EST37382 5	124	A G	CTGAGAAACAATTGGCAAAATAAAGGAAATTTGGCACTCCCACCCCCTCTTCTTCTCCCTTGGACTTTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAAACCAGCAACGAGAAAAGAAGG[A/G]CCCCAGAAATCACAGGTGGGCACGTGCGCTCCGTCTCACCGCCATCTCCCTTCTCACGGGAATTTTCAGGTAAACT
ESTD-IGFBP1	43	C T	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGC[C/T]CTGGGAGAAGAAGGAAGATGTTCCAGGGCACACACATAGCTTAGTGGGAGACTC
ESTD-IGHV4-6	120	C	TTTACTATTTCAATGGATACAGAGATTGTGGGAGTCACTACTATATTCCTATGAACAAAAAATTCAGATTTCAGTGTTAAGTAATGTTGCCTACCATTGTGTGAGTGAGTGACGGGGCCAGTGGTGGATCCGGAGAGTGTGTGGGTGCACGGACATAAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGTATGTAAAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110	A G	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTATTTTTGAGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCTCTGCCTCCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGCACCCGCCACTGTTCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	99	A G	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGTGGGTCTCTACCTTGGGTGCTTGGGTGTTCTCTGCCTC[A/G]GGAGCTCTGTCTCTGTCAATTGCAGG
EST74082	134	A T	TCCAGGGTGGCTGGACCCCAGGCCCCAGCTCTGCAGCAGGGACCCCCAGGCAGCAGGGGCTCGTGAAGCATGTGGGGGTGGAGCCACGTGTCCTTCAGCCTGCCTTCAGCCTGCCTCCCGTGCCCCTGCGCCCTGTC[A/T]CCAGATCACTGTCCTTCTGCACGGTCTTGGCCATGGCCCGGCTGGCCTGCCGCTCTGGGGACCCTTTGTGAACCAACACCTGTGCG

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EST45311 0	151	C	T	GCCCTCCTCTCTTCCAATTCTGTCCCCTATAGTTTTCCTCTATTAAGTGAACTACACATGCATTCTTTAGT GGATAGATGCACACAAACACAGACCAGCCATTATGGGAAGGATCCACGTGTGTGGCCATTATGTAACA CATTTTCTGCAAAT[C/T]ACCTCTTCATTTAACAGCCCTATTCATTGTCATTTGTTGAAT GTACATACACACATCTGTGTCATTGTTCA
EST65258 8	80	A	G	TGCCCCATCACGCGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCC[A/G]CCCTCAAAATGACAGCCATGCCGCCGGGTGCTTCTGGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGAGGGGGTTGAGGTTGGT GAGGTTAGGTGCGTGTTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26	A	T	ATGCAGGATGAAGGTGGACAGGGAGG[A/T]GAGGGCCAACCTGTCATCCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149	G	T	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCATTGTTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTACCTTAAATGCTTATTTTAAAATGACAGTGGAAG TTTTTTTTCCTC[G/T]AAGTGCCAGTATTCCCAGAGTTTTGGTTTTTGAACTAGCAATGCCTGTGAA AAAGAAACTGAATACCTAAGATTTCTGTCTGTGGGGTTTTGGTGCATGCA
ESTD-KRT10b	183	C	T	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAAAATGCATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTCTTCTAAG AGAACTGTACATGACAAATATTGCCATTCAACTATGTACTACACTATATAAGTTATAACCAGTATTAGT CTCTGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT10a	133	A	G	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAAAATGCATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTCTCTA[A/ G]GAGAACTGTACATGACAAATATTGCCATTCAACTATGTAGCTGCTCTTTTAAATAGTC TCTGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT8b	231	C	T	ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCCAGGTTTACCA[C/T]GTCAACATTGACACA
ESTD-KRT8a	21	C	T	ACCCTCACCCCTCCCTTAGCC[C/T]GTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGAACTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATA GGCTGCCTATCTCTCCCGTCTCCAGGTTTACCAGTCAACATTGACACA
EST75099 6	82	C	T	CACTTGTGTGTCTAGATCTCTCCAGTGACATCTCCAGTGGCCGCCCTCTACTGGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGGATGTCAA[C/T]GGGGGCAACCGGAAGACCATCTTGGAGAGGATGAAAGAGGCGTTGGCCCACC CCTTCTCCTTGGCCGTCTTTGAGGTGTGG

Gene	Pos	Allele	Sequence
ESTD-LF79	142	A / G	GGGTGATTTGAGGGCTCAGTTAATATTTCAAAAATTGTAACCGTAGCAAAACTGCATTGGTATTAGA AAAATAAAAAAATTTCCAATATGTAGTGCTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACC[A/G]GGAGGGGCTTCCCTTACCACCAGA
EST358799	142	A / C	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACACAGATTCCTGGAAGCAGCACAGCGGGATGGGGGCAGGAGGAGAAGAGCTGCCTGGATGA A
ESTD-LMP2	35	C / G	TACACACTTCCTTACCCATTCACTGAAAACGACT[C/G]GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTACTATGATAAGCTATTTGGTG
ESTD-LPL	113	C / T	TGTCAGTGTCCCCTAGGGGCACCTCACCACTCCCAGCTTCTTCAGCTGTCTGGCCTGTCCTGTCCTGCTGCCTGCA AGGGTTTGCTTAATTCTCAATTCAATGTCTCTTCATCTTTAG[C/T]AGCTGTGGGGGTTTGTTGTTG TTCTTCTGTTTTTGCTTAGTATCTGACTACTTTTAATTATAAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	45	C / T	TTGTCAGGAGTGTGTGCTGATGCTGCCTCCCCAGCTGCTGCCTCCCCAGC[C/T]GAACTTCAGGACAACGTGC AG
ESTD-METH	118	C / T	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTCAAGTAAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAGGGTTTGGTCTAAGTTGCTGATTACC[C/T]GGATTTTTCTGACG ATCTTTCAACTGCTAGAGCATCGGTTCCTGTTTAGCATGG
ESTD-NF1	25	A / G	ATTATCCAGATGAATTTACAAAACT[A/G]TACCAGATCCCACAGACTGATATGGCTGGT
ESTD-NFKB1	107	A / G	AACAGTGGACTTGTATATTTGTACAAAAAAAGTTTATTTTTCTAAAAAAAGAAAAAGAAGAAA AAATTTAAAGGGGTGTACTTATATCCACACTGCCACTGCCT[A/G]GCCCAAAACGTCTTATTGTGGT AGGATCAGCCCCTCATTTGTTGCTTTGTGGAACTTTTGTAGGGGACGAGAAGATCATTGAAATTCT GAGAAAACTTCTTTAAACCTCACCTTTGTGGGGTTTTTGGAGAAGGTTATCA
ESTD-NPPA	45	A / G	TGTCCCTAGGCCCAGCCCCTGCTTGTCCCCTGGCTTATCTTC[A/G]GTACTGCAAAGAGAGAACACA GACAT
ESTD-NRAS	202	C / T	GTGTTTTCTTAATCTTTTCTCCAGGAACACAGTGACCATATTCTTCTTCTGCGAGGCATATAGAATTTGGT GGGTTTCTTTTCTTTATGTGAGGGTGATATTGGATACTTTTGTTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTG[C/T]ATTCCCTGTGTGGTTTTTAATAAAAT GCCACCACCACCCCACCCAGCACCTCCAACCTCAGCCAGACAAGCTTGTTGACAAGAGAGCCC TCAGGGGCCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTCAGCCGTGTATCATCGGAGGCGGCGGGG CACATGGCCAGGGATGAGGGAAAGACCAAGAGATGCCTCTGTTGGGCCCAAGTCCTAGACAGACAAAACC
ESTD-PAI1	100	A / G	TAGACAATCACGTGGCTGGCT

Name	Pos			Sequence
ESTD-PAR	120	A	--	CTCTTCAGGAACCACCAGTCTTCTTACCAAACACGACTTATTGCTGTCGTCCGAGAGGTACAACCCGTGAGA ACTTCTTCCTAACTGTAATTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTCATTAGCTCTGTGAGTGTTTCTTCACTTTCTGTTCTGTTCTAGAACGTTTTCTAG GACTGGCAGTTAAGCTTCACTTAGGCTTCGTTTCTGTATACCCATGCC
ESTD-Per/RDS	74	A	G	ACCTACAGACGTCGCTGGATGGTGTGTCCAACCCCGAGGAATCTGAGAGCGAGAGGCTGGCTG CTGGGAGA[A/G][G]GAGCGTGCCGGAGACCTGGAAGGCCT
EST68308 5	29	C	T	GGAAAGAGATTTAAGAGAGCTTGGA[C/T]AATTCTGGTTCTTTGAGTGTGGAAGAGTTCATGTC TCTGCCTGAGTTACAACAGAATCCTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST54045 6	39	A	G	GGAATATTAAAAATATTTTAAAAATACCTCCATTTGCTT[A/G]TCCTTTAGTGAAGATGATACCTGC AAAAGACATGGCTAAAGTTATGATTGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTGTTTGCCTTGGAATTGGATTTTTAATGTTGACTTTATCAT
ESTD-PXMP1	88	A	G	ATGAAACATGGTTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAAGGGGCTTCTTTTTTTA ATGCAGAAAGAGGGGAAAAA[A/G]GAGCGAGCTGTGGTGGTGACAAGGTGTTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAGTCTATGAAATTATAATCTT CCCGAGGAATCTGAGAGCGAGAGGCGTGCCGGAGAAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTCTGGAGAGTGTGAAGAAGCTGGCAAGGGCAACCAGGTGGAAGGCGCGAGACGCCAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-RDS	127	A	--	TTGGGAAGTTAGAGCCTATATTAAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTC[G/T]CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
ESTD-s14544	94	G	T	ATCACAGGTCTCTGGTCTCTGGCCATCATTCCTGGGAGAGATGG[A/C]TGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST52908 0	45	A	C	AGGAGAAGCTGAGGAGGGGAAGAGAGAGACAAGAAGAATGACACATTGATGAGTGAAGATGT[C/T]GGCTCAG GATGCCGGAAAATGAC
EST19590	55	C	T	TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACC[C/T]GCGTCATACCTTTATCTATAGCCTT CCCCTAGGTCTT
EST76136	39	C	T	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTGTTTCTCCTGGGAGCCTGAGGAGTTTGTTGTCGTGTGTG CAGTCGCCCCGCGCCACCTGCTTGAGCCTGGTTGAGCCTGGACATACACCTTCACCTCCTTGGCCCGGAGAAGAC ATTTACCCCACCTGGCCATGTCCCTGGCCGTTGTGCACA[C/T]CCTCTGTGAAGACCCAACCCCTGC
ESTD-SPTB	176	C	T	CTCCCCCACCCAGCCAAGCCAGTTTCCTAGCAAGGGCAGGAC

				Sequence
ESTD-TAT	224	C	...	AAATGGTCAGGACCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAAATGACTTGTGGGACAGGATCA ATTTCCTCTCACCTAGAAACGTTGTTTACAACTTTTCTTCCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAATTTAAATAGGACCCATGAGACACATCA
ESTD-THRB	125	A C	...	TGCGGCCTTTCCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAAGAGAGAAAGAGTCCCAAG CACACGAAAACAGAAGTTGCAGATCCCATGAGGCCCAGTCTCAAATCACACAGGATC[A/C]CTTCAT CCACACTGGATTGGCCCAAACAAGTCTGAGTGCCAGCCAGGACTCACGGTCCCCCTGAGATGGG
ESTD-TYR	122	G T	...	TAGTGAAGTTTTCATCTCCTGTCGTCTTCTGGATTTCTTGTTCCCACCGCAACAAGAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTGCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCA[G/T]ATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGAACAAAGAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYRP1	222	A C	...	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAAGTTCTAGGCATACTT AATACAAGCACATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-TYRP1	222	A C	...	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAAGTTCTATTTTCTTCACTTATTACCTTCTTTCT AATACAAGCACATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-VB12	148	C T	...	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-VB12b	148	C T	...	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-VB12a	74	A G	...	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCA GTGACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

ID	Pos			Sequence
EST58607 0	105	A	G	CTCTGGATGGGTTCACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAGGACAGCCAC[A/G]TGGGCGGGGATGGCCGGGCGGGGAGTTC TGGTTGCGGCCACGGCGTGTGGCCTTCGTTGTGAACGGTAGCCTTGCGGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAGGAGGGGCGGGGTGCCATGCCTGAGATGCGGCC
ESTD-VWF 36		G		AGGTAGGAAAGCAAAGAGAGTTGATTAGTGAAGGAGGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
EST71770 6	189	C	G	AGCACCACCTCTCAAGCCTCAGCGTGTGTTCTATAAGGATGACGTGCTGTGTTTACAA CATCTCCTCCATGAAGAGCACACAGAGTTATTTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTTGGTGGGA AGGAGTGCCCAGTCCCAGGGTGACACTGGACAGAAAGAGGCCATCCAAGG
ESTD-TNFAb	152	A	G	TTCCTGCATCCTGTCTGTGGAAGTTAGAAGGAAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGGTTCAGCCTCCAGGGTCCTCACACAAATCAGTCAGTG GCCCAGAAGACCCCCTC[A/G]GAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG CTTGTGTGTCCCCAACTTTCCAAATCCCCGCCCCCGCGGATGG
ESTD-TNFAa	88	A		TTCCTGCATCCTGTCTGTCTGGAAGTTAGAAGGAAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGGTTCAGCCTCCAGGGTCCTCACACAAATCAGTCAGTG GCCCAGAAGACCCCCTCAGAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCCAACTTTCCAAATCCCCGCCCCCGCGGATGG
EST52418 6	113	A	G	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGAGCCTACAAGATGTCG GGGAGTGGCCGGGGAGTTGGGCGGGAGTTACGGGCGTGCAGGCATCACACT[A/G]AAGTGAAAACTGTGAGTG TGG
EST13586 3	89	A	G	CCCACTCTATTTGCCCAGCCCAGGGACAGAGCTGATCCTTGAACTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[A/G]GGGCTGGCTTATCAGCCTCCCAGACCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGCCTCTTAGAGACTGCGCAGAGAGGTGCGTCCTCGCTGCCTGCC CCGGGTCACTC
EST51976 7	123	A	T	AGGCAGAAACTGGGCCCCCATGCGGGGGACGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[A/T]CTCTCTC CCTCCCTGAGCTGGAGCTGGAACAGCAGGAACAGCAGCAGGAGCAGGTGCAGATGCTG GCCCCTTTGGGAGGGATGAGAGCTGCCCCTGGTGC
EST11458 6	140	A	G	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTGCTCATCTTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACCTGTCCCAGCCCAGTGATTACCATTTCCACAGTGGT CCC[A/G]TTAAAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTG TCCCGGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

				Sequence
ESTD-AT3aa	60	C	T	AGACCTCAGTTTCCTCTTCTGTAAAAGGGAAGTTTGTTCTTGGGATCTCCATGGGCCCAGC[C/T]AGCA CTGGTGCCCTGTGAGTCTGTGTATCCAGGTAGAGAGGATGGGACCCAGGTGGAGGGAGAATTTGAAAAGGGCA TTGGAATTCAGAGACAAAGAGACAGATATTAAGAGCTGGGGAAATGTGG
EST398528	106	C	G	CGGTCTTCCTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGAAGCATCCATAAG GCATTTCTTGAGGTGAGTACACCTCCCCACTCTCTTA[C/G]GGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAAGGCCTGTTCCAGTGTTAAGGCGATCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST624480	112	A	G	ACCTGGTGCTGCTGGTGGGTGAACCTGGTCCTCTTGGCATTGCCGGCCCTCCTGGGGCCCGTGG TCCTCCTGGTGCTGTGGGTAGTCCTGGAGTCAACGGTGCTCCT[A/G]GTGAAGCTGGTCGTGATGGCA ACCCTGGGAACGATGGTCCCCAGGTGGTCAACCCGGACACAGGGAGACGCGGGTTACCC TGGCAATAT
EST360272	120	A	C	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGGCCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGG[A/C]AACCTGAAAA AGGCTGTCATTCTACAGGGCTCTAATGATGTTGAACTTGTTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGGAAAGACAA
ESTD-COL2A1cc	112	A	G	AGAAATGTATATAGTCCTCAAACTGGCCATCTCCATTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTTCTGTCACTTTC[A/G]GGGTGTTCAAGGTGGAAA GGTGAACAGGGGTCCCGCTGTGGTCCTCCAGGTCCTCCAGGTAAGTCAACTCAAGCATCAACATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1dd	97	C	T	TGAGAGAACACCTAGTCCTCCATCCTTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACA[C/T]TTGGACTTCTTCTACTGCGACAAGAGACTTA CCCAAGAGAGAGATTAATGGCAAAGATATACAATTTTATTTGACCAAACACTATCATGGAACACA GCATT
ESTD-CPT2	150	A	G	GCCGCAATGCCCGGGGAGTTCTCCAATGTGTGGAGAAGGCCTTAGAGAGACATGTTTGATGCCTTAGAA GGCAAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCCTCATCATGAAAAC TGGGAGGCCGGCGGCAT[A/G]GTGCTCATGCCTGTAATCCAGCCATTTTGAGAGGCTGAGCGGGGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST122740	135	A	G	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGTAAGTCAAGTGGTTTACTCCTCATGACCAAATATTCTTCCCTCCTTAGGATGAGGTG[A/G]TAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCCATGGAGGATACTATAACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91	G		ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCTCCTATCTCCAGGGCCCTGTCATC CAGCTCACTCATCAATGGGCCCAGTCAGGCCCAGGCACTGCAGGGTCCGGAGCACTCACCCACTGCCCCT GCTGCCATGTGGACTGGTTGCAAGTTGAGGACTTCTTG

Name	No.	Allele			Sequence
ESTD-SSA1	111	C	T	---	TTCACTTTGTGGATTGTTCTTTGCTGTGTGCAGCACCTTTCAACATGATGTGATCCCATTGTCCAAG TTTGCTTGGCTGCCTGCTGCTGTGTGGGATATTGAAAGAGAT[C/T]TTGCCAGTCCAATGTCCTAGA GAGTTTCCCAAATGTTTCTTGTAATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATT TTGATTTGATTTCTGTA
ESTD-RYR1	109	A	G	---	CTTCGTGACGGGAGGTCACGTCCTCCGCCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGATGACGCAGACTTGTCTACTCATGAG[A/G]GGGGAGCTGTGTGCACTCATGCC CGCTCCCCTGGAGCCTGGGAGCCACTGAGAATCAGCTGGAGTGGGAGCCACCTGCGCTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTCACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70	A	G	---	AAGACCTACGTGAATGTTCACATGTCTTAAAGCCTCCCTTCCTCTTACTCTCTGCCTGAGGATGTG CG[A/G]CGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2	100	C		---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCCTCCAAGGCCGTAGGGGAACTGGGGGATCTAGGGGTGAGGGAATGGCCC AGCCCAGTCCGGCCCGGGCTGCCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGGATGGGC TGGATGAG
EST444387	62	C	T	---	GCAGCCAGGAGGCCGCTGCACCATGCCCCGCATAGATGCGGAACCTCAAGCTCGACTTCAAGGA[C/T]G TCCTGTCCGGACCTAAGCGGAGCGGAGCAGCCTCAAGAGCCGAGCCGAGGTGGG
ESTD-PBDA	103	A	G	---	CCTTCTCATGCCCAGATGGAAATTCCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGGTGGCTGGGAAAGGGCAGGACTAATCCAA[A/G]TCTCTACCCGCAGCTTGCTCGCATACAG ACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
EST128393	122	A	G	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCTCTTGCT CCTAACACTCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG[A/G]TCAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGAAACTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTCAGTATGAATTATTATGTAGTACTTAGCTTAG
ESTD-CTLA-4	48	A	G	---	ATGGCTTGCCTTGGATTTCAGCGGCCACAAGGCTCAGCTGAACCTGGCT[A/G]CCAGGACCTGGCCCTG CACTCTCCTGTTTTTCTCTCTTCATCCCTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCATCCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
ESTD-ACE	96	C	T	---	GATCAAGCAGTGCACACGGGTCACGATGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC[C/T]GTCCCCGCTGCTGGGGGCCAACCCGGCTTCCA TGAGGCCATTGGGACGTGCTGGGCCGTCTCGGTCTCCACTCCTGAACATCTGCACAAAATCGGCCTGC
EST544198	88	A	G	---	CTTCTGCCTAATTTGAATGATATGTTGCTGGTGTGGAGACTGAGCACTTTATTGGCACAAATGATCACTA TTTCTTGACCCCTACTTAC[A/G]ATCCTGGGAGATGTATTTGGGTTTAGCCGTTGGTCGTATGTTGTCTA CTATAGTCCAAGTGAA

				Sequence
ESTD-PS-1	99	A	G	GGGGAGTAAAAACTTGGAATTGGGAGAGATTCATTTCTACAGTGTTCTTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACAACCATAGCCT[A/G]TTCGTAGCCATATTAATTGGTTTGTGCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD-B3AR	104	C	T	GGCTGCCAGGGGTTCCGTGGGAGGCGGGCCCTAGCCGGGCCCTGCTGCGCGCTGGCGGTGCTGGCCACC GTGGGGAGGCAACCTGCTGGTCATCGTGGCCGCCGACCTGGTGGCCATCGCC[C/T]GGACTCCGAGACTCCAGACCATGACCAA CGTGTTCGTGACTTCGCTCGCCGCCGACCGTGGTGATGGGGACTCCTGGTGGTGTCCGCCGCGGCCA CCTTGGCGC
WI-567b	48	A	G	TCTCACACTGACCCCTTACCTTCACCTCTGCTGCCTTGGTTC[A/G]AGCCCTCATCTCTTTA CAGGGGATCCGCGCCACAGCATCCCAACTGATCTGGCCTTAGTGTCTTCTCTCCAATCCATTCTTCAAAAG GCTGCCACTGTGATCTTCCCAAAGGTGATTCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58	G	T	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCT[G/T]AGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCCTCAGCCCACCAGAGAGTTAA CATTTCTGCCACCCTC
WI-801b	58	G	T	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCT[G/T]AGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCCTCAGCCCACCAGAGAGTTAA CATTTCTGCCACCCTC
WI-1099b	76	A	G	GAAATTCACCTATACAAGAAACTATTTCTCTAATTATTACATTAGTCTCATTATTCTGAAATATTAT TTTTACA[A/G]TACCCTTGATTATTTTGATTATTTCATTGTAACGAGAGATTACAATATCAGTAACGC TGTTCATTGATAGTGCTATCACAAATGTCTAAAATACTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGTTTA
WI-2529	71	C	T	AGGAAATGGCTGATACTCCTGGTGGCTTCATTATATGTAAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA[C/T]TCTTAACTGCTGCCTCAGTCAGTGAACATTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAAATGCTAAGCTTGAAATAAAGTGAAAGAGGTAAAGAAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTCATTAGAAATGGCTTGGGGATGACAAGTA
WI-10088	205	C	G	TAAGGGCCTGTCTTCCCCCAGAGGCCCCACGGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGATAACCTGTACCTGAGGTAACCTGAGGATGAAGGA GTGAGTCATATTGGGGTGGCAATTAAATGACCCAGCCTCCTCTCCAAGAGACTTTACATTTTAGAC AGGC[C/G]AGCAGAAGCAGCAGAAGGAGAAAGGAAGT

ID	Pos	A1	A2	Seq 5′	Seq	Sequence
WI-2625	98	G	A	---	...	GGGCAGTCCTGGCTGTGAGTGTAGACAGCACTGAAGGATGGGAGGAAGAGAAGAAACAGGCAGAAGCACTGTGGTAGTTAACAAGGCTTATTAGGA[G/A]CAAAATTGATGATACTCCCTGAGGACTCGCAGAAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCCACTTGCAGGAGGAAAGCCAGCCAGCAAAG
WI-2924	54	G	A	TGACCTTCCTAGTCTTCTCTTATAGG	GCCCTAAGTGTAATCACAGGG	TCTGTTGTCATATTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG[G/A]ACCCTGTGATTACACTTAGGGCCTACCTGGATTATTAGAACAATC
WI-2939	72	G	T	GGCTTGTCTCAGTGCCTTT	CTTGTTGAGGGAAGGTCTTG	CCATTGTTGAGGTTGGGTGGGTCACTGTCATTCCCTGCCACTCAACAAAGTGGCTTGTCTCAGTGCCTTT[G/T]CAAGACCTTCCCTCCACAAGAATGTCTTCCATGCTCCCGTGTTCTTTGAAAATTCGACTTTATCCTGAAAAACTCAGCTGCAGTGTTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99	G	A	GGTTATGCCGCAGACGAG	TCAAGTATTGCCTTGTGTGG	CTTGCTACCATGCATTCACAGCATACAACCCTGCAGTGAAATGCCGTAAACCCCCATTATAAAACATCTTGCCATCGAAGGGGTTATGCCGCAGACGAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGAGAATAAAGATTTTGGATGGATGAAAGCAGAGAAGGAGATGCTAAAAGTGA
WI-3473	101	A	G	AAGCATTTTAGCCCTAGGGA	CCTGATGTCACCAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGTAGTTGGTATAGGCCCTGTTGGAGATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[A/G]TAGAAAATGTTGGTGACATCAGGGCT
WI-1796b	29	A	G	---	...	ACACACTTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCGTCATTTCTGCACATGGTGATATTTAAGCAGGAGAGCATTGTCTTGGCTCCCC
WI-1796	29	A	G	---	...	ACACACTTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCGTCATTTCTGCACATGGTGATATTTAAGCAGGAGAGCATTGTCTTGGCTCCCC
WI-4360	93	C	T	GTAGTCACATTAGGTATTTTCCTAAAATAA	GAGAGATATTTTCAGAGGCATTTT	AGTCGTCCATCTTCAGGGTCTAACTCTGGACTCTGGCCTGCAGAGTAGGAGAAAGAAAGATGGGGTGAGTAGTCACATTAGGTATTTTCCAAATAA[C/T]AAAATGCCTCTGAAAAATATCTCTCCCATGTCCCTGTCTAAATATAAACATTTTCCC
WI-1959b	87	C	T	---	...	GCTGAGCTTTGTGCGCAGAGCCAGGAGCACCAGGGACAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAACAGGAACCAAAAATCAGTC[C/T]GGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1973b	28	A	G	---	...	GTTGTGCCTGTAGCAGACACACAGAAGGCA[A/G]AGAGGAAAAAGCCTTTTTGGTCAGGGCTTACACTGAATCCCTCAAACAATGCAAGATGAGCTAATCTTAGAGGTATAATCTAAGTGTGAGAAAAACAAAGGTATAGGGTTTG
WI-1980b	140	C	T	---	...	CTTGAGTAGTGCGTGGATTTTGGTATACACAGAAATGGGAGGAGAGCTGGAACTAATCCCCCATATACCAAGGGACAAAAATTGTATCTGTTTCTACAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAATTTTTAA[C/T]GACAGTTTTAATTGAGTGAAATTAATAATAAAATAATAATAGCAGCTAATATTTACTGAGCTGTTACTTAGGTGCCTATAAATAGC

Identifier	Pos	Alleles	Sequence
WI-2015b	190	A G	---	TGTCAGATAGTCCGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCTATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCCAAGACTATGTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACACTTGGTGCTTTTCCAACT[A/G]CATATACTTCTAATACCCATAGAG
WI-754b	49	C T	---	GAAGGCACAGGGAGAAGATGGCTGTGTCATCTACCAGCCAGGGAGAGAGAAGC[C/T]ACATTTATTGGTAATCCTATAAAGTGCATTCTTAAAATTGTATTTACTTTAGA
WI-754	22	T C	---	GAAGGCACAGGGAGAAGATGGC[T/C]GTCATCTACCAGCCAGGGAGAGAAGCCACATTTATTGGTAATCCTATAAAGTGCATTCTTAAAATTGTATTTACTTTAGA
WIR-1b	56	A G	---	AGGCAATCAGACCTACAGAAGGAAACCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGCGCTGGAGGGTGATGCCTCCTGAGGGACATGGGAGCTTCATGTTTGGAGCCCTCCTG
WIR-1	56	A G	---	AGGCAATCAGACCTACAGAAGGAAACCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGCGCTGGAGGGTGATGCCTCCTGAGGGACATGGGAGCTTCATGTTTGGAGCCCTCCTG
WIR-3b	72	A G	---	TAATTTTAAAATGGGGCCAATAACACAGTACTTATCTCACAGCCATTTCTCTAAAGGCTAAATAAGAAGAAGT[A/G]TCTAAAAGTTATTAGCTCAGTACTGACTGATAAACAATAAGCAAAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A T	---	TAATTTTAAAATGGGGCCAATAACACAGTACTTATCTCACAGCCATTTCTCTAAAGGCTAAATAAGAAGA[A/T]GTATCTAAAAGTTATTAGCTCAGTACTGACTGATAAACAATAAGCAAAGCTGGGTGCTGAGATAAGA
WIR-4	47	T	---	GAGCCTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCAAGGCAGCAGCAAATTTGCCCAGCTGCC
WIR-5g	209	C	---	CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5f	196	C	---	CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5e	194	C	---	CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG

Marker	Pos	Alleles	Sequence
WIR-5d	191	A ---	CGGGACAGAGAGACAGAGAGAGAGAGAGTTCTGCGAGCATTCACAGAGAGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGAGCCTGTGGTCCCACTGTTAGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5c	177	C ---	CGGGACAGAGAGACAGAGAGAGAGAGAGTTCTGCGAGCATTCACAGAGAGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGAGCCTGCCCAGAGCCTGTGGTCCCACTGTTAGGTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5b	159	A ---	CGGGACAGAGAGACAGAGAGAGAGAGAGTTCTGCGAGCATTC[A/G]CAAGAGGTTATTAGGACTCAGTTCTGCTGTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGAGCCCAGAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5a	37	A G ---	TAACCCTGAAACTTTGTCTTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C]CGCCAGTCTTGGGGTTGGGGCAG
WIR-6	63	A C ---	TTCGTTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGGAGATTGATC
WIR-7	12	C T ---	GGGGTCCTATGACTATCCTGGTCATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-8	46	C T ---	AAACAGAAAAATAGAGGTTATAAGGATGAACTAAAGTTGTCAGAAGAGGTATGA[C/G]CTGAAGAAAGAATTACTCTCTTTGACCAATAAATACAATTGGGAAAACCATGGCTTGATTACTGACAAC
WIR-2	56	C G ---	TGTCCTTGCTTATGCCTGCCTCCTTTGCCTTGGCCAGGATGATGCTGTCATTAGTATTTCACAGAGAAGTAGCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTTACATAAAATAAGAGATCCTTTAGTGCAACCAGTGACCATCTTAACACAGCCGGTGTTGTTCAAATGTACAGTGGTCCTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93	G A ---	GGTCATTTCCTTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCCCCACATACCAACTCTTCCACCATGATGATTATACCAATAAATACAGTTCCTTATATGAGGGGCTCTGGAAAATTAGACAGTGAAG
WI-18694	41	A T ---	CACACTGTTCACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTATTCATGAAGAATGCATAATCTCTGAAAATTATGAAAACATCCCT
WI-18612	37	A G TGC	CCTATATTTCA AGTTTGGAAA AGTTTGGC TTGTATTGCTG CTTGCAAAT

ID	Pos	A1	A2	Seq A	Seq B	Sequence
WI-18517	87	C	T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAAATCAACTAGGGCTCACCCTCAACACCCCCCTCAACACCCTCATTTGTCAACCTCTCACAGCCTCGCATGCC ACAGGAATCAGCAGCAGCCTGA[C/T]TGTTGCACTTGTCCAAACACAACAACTGACTGC
WI-18668	76	C	T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTAAA CTGCACTTTTT GC	CGATTGACAACCTTTATTTCAACTTAGGTAACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAAA[C/T]AGCAAAAAGTGCAGTTTAATTTAGCAAAGGCTCAAGACAGTGTGGAAGGAA GGTGAGATTTCCCTCCTACT
WI-18680	75	T	C	GCTGTGTCACTCT AGCATCTGGA A	CCTCCTGAATA TACAACGGAGC A	TAAAACATACGAGTACTGTACACGCAAGCAGCATGCATCCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[T/C]GCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGTTCTCCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGGAGCACCACCAGGGCACCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC[A/C]CCAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29	A	G	---	---	TGTGGGCAAACCTTGTTTAATTGCAAAC[A/G]ACTTAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	GCAAATACCAC TGAAGAGGAC A	GTCGTGGGGTG TGAAGAGGAC A	ACCAGTCATGTGTTTATTTGGAGGTTAATTCCTATTAGGATAATGAAAGGATTCAGCAACGATTGAGATT GTGTTCCTCACGGAGGGGCTCGGGCCAAGGTCGTGGGGTGGGGGGGTGCAGAG[T/C]GTGTCCTCTTC AGTGGTATTTGCGGACC
WI-18533b	91	T	C	---	---	GGGGAGGAGGAGGTAGATTGCCAAATTGAGGGCATTTTTTTAAACTCCCGAGATTTTTCTTCTTTATTT TATATTTTCATTTTCATCCTAA[T/C]TTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
WI-18533a	59	T	G	---	---	GGGGAGGAGGAGGTAGATTGCCAAATTGAGGGCATTTTTTTAAACTCCCGAGATTTTTCT[T/G]CTTTA TTTTATATTTTCATTTTCATCCTAATTTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
D11734	83	A	C	TCATCTGATAC AACCAGGATA CTTGTTCAGAT AGGCTACAACT ATTT		GAGCCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTCAGATTTC[A/C]AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A	T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTGCAGCTGCAGACGAGCAGACAGAGCAGCTCATGGGCAACATCACTGGGCCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGGTCTTTCATTGCTAGTGACTAGCCCCCTAAATGCCAGCGCTG AGTACCTGAAGGAATCTGGGAATT[A/T]GCCCCTGCCCATCATTCATCACTACCCACTGTT CT
EST100307	98	T	C	CATTTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAAATTTT CCCTTAGCCATTTTGTTCTCTCAAGTCCCT[T/C]CATCCATCACCACCACTGCTCAGTTG
EST100522	24	G	A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[G/A]GAAGTCTAAGATTGAGGTTCCACATCTTTGTGAGGGCCTTC CTGTTGAGTCATAACCTGGTGGAAGTCATCGTGGCAAGAGAGCTACAGAGGGCTACAGAGAGCAAGAGGAA A

EST	Pos	Allele 1	Allele 2	5′ flanking	3′ flanking
EST10605 2	118	C	G	---	CTTGCGTAAATCACAGTTCTGTATTCATACAAAAACTTGTTTTCTGACAAACTGTACACATAGAAACAAATTCCAAATGGACAGGAACTTAAATTTGTGGAGATGCCCCATGT[C/G]TTGTGTGAGACTTAAAAAAAGAAAAAGATCCC
EST11048 0	61	T	G	CTCTCAAGTAG ATAAGAGGCA GTAATCT / GCTAAATTTC AGAAAGAATT TTGTTT	CATGTGTCAATCCCATGATTGAAAAGAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCT[T/G]AAACAAAATCTTCTGAAAATTAGCTTATGAACTCATTACACTGCAAACCAGAGAAGGAGCAC
EST11260 8	101	G	T	---	TATGGAGGCCAGAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCAACACAAAATTCTATATCCAGCTAAATATCATTTAAGAATGAAGAAG[G/T]GGAAAATGAAGGCAATATCAGATAAA
EST11349 9	109	C	T	CCAGCTTTCT	TTTGATGGAGAAATCCGAGGCCTGCCAGCATCCCACCAGTAGATTCTTTGGACGAAGAAAATCCTTCTGTGGGATTCAGCTTTACCGCCTTTCCTCATCTGCTGGTGT[C/T]TTCCTCAGAGCTTTAATGTCCGTCCTGCTCTCCGAGTCAG
WI-16632a	71	A	G	CCAACCTACTT CTAAAAACTCC T / TGGAGCCCT	GAATTCTGGGTATTAAATAGCGGGTGCCACAGAGGAGCACATAGGAGGAGAGCATCCAACCTACTTTGGAGCCCT[A/G]AGGAGTTTTAGAGAAGAGCTGGACGCCCGAAGACCAGTAGTAGGAGGTAGCGAGACCAAAAGGGAGGAGGAGTGGGAA
EST11772 6	74	A	G	---	CCAGGAATAAAAGAAAAAGAGAAGTCAGAGGAGGAAACAGTCTTGATGTTATGAGGCTGAGACACTACTCTTCCTTCA[A/G]GACTATTTCATTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82	G	A	---	CTTGTCCATTTATTTGTGCATGTTGTTCTTAAAAGGCTTGTGAAAGATAACTTGGAATGTGGGAAACACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42	G	A	CAATAAGCAG CTCATTTTGAT CTAC / ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGCGATCTCAATAAGCAGCTCATTTGATTAC[G/A]GGTATACATGAAGTAAAATTCATGAAGTAAAATTCATTACCAAAAAGCCTCCCACGAACTTCATGCACCCTGAGCTATGTGAACTGAAAAGTAACAGTGGGAT
EST12005 9	56	A	G	TTGTATAATA ACACTCAGTA GCAAAGTCTGT / GGCTGGTCACT TCCTGGAT	GCCTAGTAATTCCAAAAGGAACATGTTTGTATAATAACACTCAGTACAAAGTCTGT[A/G]ATCCAGGAAGTGACCAGCCCGACGTTGCTATGCACCCTCTGAACCTCCATTTCCATAGTTTTTGAAATC
EST12055 9	32	T	C	---	GTGGAAAATTTTTTATCTGTTACGTCTTTCC[T/C]ATTATATTTATCTGTCCTTGATTTCAGCACCCCACCCGATTTGCAGGCAGTGCTTTCTAAACTGTGCCCTGTGTTAAAAGTCTTCT
EST12492 1b	95	A	G	---	CCCCTAGCAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATACTGTTGCCAAAATTAAGCTCTCTTCCCCAGAGAGGCATTACTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTTACCTTTTTA
EST12492 4	25	A	G	---	ATCTTGAGGTTTCTGGGCCTGTCAG[A/G]AGTGACATCTTTTACTTACCACAGGTCAGGAACCCTATAAAGAAACTGTGTAGAAAGATATCAGGTCAGACTTTTAAAGGGCTTCTTATCAGCTCAATAA

EST ID	Pos	A1	A2	Seq (5')	Sequence
EST12502 2	52	C	G	---	ATAACTAGGGAGGAGAAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGGTTCGATGAAGAGAAAATGCTCACGGGGGAAATGACCATTTTAAGGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105	T	C	---	CCAGAGAAAAATTAGAATGTATCGGTAAAAGAAATAGGAATGCATATTCAACTCACTGTCACAAA CAGGTGTTTTATTATCCCAAATGACAGTGTT[C/C]GATGCATGTGGCAGACGAG
EST12620 0	67	A	G	---	TTTCTTCTCCTTCATTTATTCATTCATTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGC[A /G]TTGAGAATACAATATTGAAGAAGAGTCACTGCCTGCCCTCTGAAAAATCAGAGTATTTGA
EST12817 9a	22	C	A	---	TTGGGGTTCTCCAGGATTCCAG[C/A]CTCGTAGCTGAGTGCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGGGATGGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCATTGCG
EST12941 8	23	T	A	---	TCTCAGCTTCCACCTGACCTGCAT[T/A]CAACAGCCCAGTTATTCACCAGAATTTGTTTGCGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACTGTTTTG
EST12949 2a	52	A	G	GGCTTTAATCA TAACCTAATA ATACTGTT	TGTGTCCCTGT GGGTCTC — AGGATTTCATGAGGCTTTAATCATAATAATACTGTTAAAAACAACAC[A/G]TTCTGTCACTTG CAGAGACCCACAGGGACACACCATTCTCTCCTCTCCACATAGACTCTGAGGTAGGAGTACACTGGCT AAGGAATAA
EST13067 4	104	C	T	---	ATTTTTGTTTCTTAAATGAAGCATAATAAACAGTTAAAATTCTCAGAAAAATCATCTATAGTTGA GTGTAAAACTCCCCTAAATCAGTCTTCTAGGGCCACA[C/T]TGGAGCAGAAGCAGCTTCCCACCCAAG CACCTCTGAACT
EST13117 6	66	A	G	---	TGCTGTCTGCATCAGTCCTTTAAAAATTTAATCGCTTTATACAATTGACACCAAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTGAGAAGCTGACACGTGTCCATACAGACACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44	C	T	---	TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTTGTTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACAATTCCCTCCACAAATATTTCCTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74	T	G	---	AACTGTTTACTAACAACAAGGTGCTTTAATTTGAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATTT[T/G]GACTAACCAGTTCTACAAATTTCACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72	G	A	GCTCAGATGTG AGAGACGC	CCGGCTCCTGT ACAGAGA — GCATCATCAGCGGCTTTTACTGAACTTACAACCAACTTGCCGCCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCGTGTACAGGAGCGCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCAGGCA AACAGTTTACTCCACAT
EST13236 9a	70	T	C	AACCAGATTT TCTCAGGCCT	ACAAGAGGGTT TGACAAAGA G — AAAGATATAAAAACAACTCCCATCAGTAGCAATACAAGGTATACATTTTAACCAGATTTTCTCAGG CCT[T/C]TTGGATACCTTTAGTAGTTAACTCTCTTTGTCAAACCCTCTTGTATATAACCA

EST	Pos	Allele 1	Allele 2	5′ flank	5′ flank	Sequence
EST13278 2a	51	A	G	CTTCACCGAA CAATATTTTAG	CATATTCTGG GTGGTGAGAA	TTCGCAGAACGTTTACAAGCTCCAAACCTTTCACCGAACAATATTTTAGG[A/G]ATTTGAAATTAT TTCTGTAGTTCTCACCACCCAAGAATATGACAGCTTG
EST13282 0	99	A	T	CCACACATTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAATATTAGATAATACCTGTTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAATCCCACACATTTCCATCTCCCAAATTTCCATCTCCCATCAGA[A/T]AACCTTCCTCAAATTTCCATCATCTCCCATCAGA GG
EST13290 9	39	A	G	CAATTTTAGA AGTTTGGGGTTT	AAATCACTTCA TGGAAATTTCA G	AGCTCATCTGCAAGCAATTTTAGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTTT TTTTCTGTGCTTAACTTCAGTTACTTAAAGACCTAAAAGACAAAGTGGTATCACATCACATATTTGT ATGTGTGGGCTTTTTTG
EST13518 2	45	C	G	---	---	GAAACATCCTCCAGTAGTATTGAGGTTAAAATGATTCAGCATTTA[C/G]ACTTTAAAAAATTACCTCA ATGTTCCTCGGAGTCGTCGTCCATAGTTTAAAATGACTTCTGCACCTTCCTTATAACCTTGATTG
EST13522 8a	66	A	G	---	---	CAGGTTGGTGATTCTCAACTAGGAGCTATTTGCCCCCCATCCCCACCCGGCAGTGTCTGGAGAC[A/ G]GTTTGATTGTCACAACTGCGAGAGGTGGGTCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69	T	C	---	---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAAGGAGGTTCGGTTAGTTGAGGGAGAAAGTTGGAAGCA TTTTCAAGCTAAGTAAATGGT
EST13785 0	101	C	G	---	---	AAGATTACGGACCACATAAGAACTGCCCCCCGACCCATACACACACAATTTATAGCAGGTAAAACCAA CTGAAAGGAACAAAGTAATGACTTTCTTGAACAAA[C/G]TGATTACGAAGGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A	G	---	---	CCTCAACCATCTGTAACCCGAGCCC[A/G]CAGTGACCGGGACTTGCTGCTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23	A	G	---	GGAACAAGTC	CAATGGTGTCCATGTGAACATAT[A/G]ACCTATTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGGAAAGTCATCTGCTAAAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	42	T	C	GCATGCTAGA CAGAGGCATT	AAAATATTTTT AAAAGA	AATATCAATGCATTCTTGTTGGCATGCTAGACAGAGAGGCATTA[T/C]TTTTGAAGATCTTTTAAAAAT ATTTGACTTGTTCCCCCTTCACACTCATTTTTAAATTGT
EST14812 2	50	A	G	CAAGTCAGCTT CTACATTCTGA ATA	TAAAGATTTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCTTTCAAGTCAGCTTCTACATTCTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTGCCTTTTCTAACATTTTCATATCAGGTGAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128	A	T	CATCACCACC ATACTGGTT	CGGGAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGCGCAATGCAGCGTGAGTTCGCGCCGTCTCCCCACTGAACCAGTAAT TCACCAGACAATGGCGCACCACTAAAAATAAACTTGCCCGTCATCACCCACCATACTGGT[A/T]TTCC GGTACTGTTTCCCGTA

Clone	Position	Allele 1	Allele 2	Sequence
EST15420 6	109	C	A	TTTTAACCCCAAGAGACTTGTAGAGTGTCAGGACTCCGATCATTTCTCTGCCTATAGCTTGGATATCTTAATCTCTCCCCTTTGTCATCATAATCATATAGCCAAGGACT[C/A]GGAATTTGGCTGCTTCAAGTCATTCCAAACCTCTCAGG
EST15700 6	48	G	C	GTCACCAGCACTTTATTAAGACGTGAAAAGAGACAAAGAGAGACAACAGAGGA[G/C]AGCAGAGAATAATATCTCTGTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCCTTGATCTGATGTAGTA
WI-16739	57	G	A	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAGC[G/A]TTATAGGGAATAATGAAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAATTGCCTCCAAGGT
WI-16782	96	C	T	CTTCTTCCTTCCTGACGCTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGACCATAATGGTGGGAGTCTCACTGTAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGTGCTGATGAAATTGTGGGG
WI-16783	64	A	G	AAAAATGTAAAACTTAGAGGTTGCCTCTTTTGTGTCACTTTCCTGAGATGTCTTTTACCTGAG[A/G]CTAATAAGGATTGAACCAAGCAGTATTTTTTAATGGCAAAGTCCAGATGTAACTCGAGT
EST15948 2	58	T	C	CAGGACTTAAGGTCATTTGCCTGGAAGACTTAACTAAAGGTCAGGGCAACATAGGA[T/C]GTGACAGCAGCACCACTCGGACCAGGAAGTGCTGAAATCGTCACACTAGCGGTGCCCAGCCCCTTTTTCCTGGCTGCTCTGCCTCCCCAGAGC
EST16088 8	89	G	C	GGTTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGGATCTCATTTGAGAGCGTGTTTTGTCAGCCTTTTCCAGAAAAGGCCGCTC[G/C]GGGGTTTCTGAACCCTCTATGGGCATTTTAGAAT
EST16089 9	96	C	T	CGTCTGAAGTTTTTCTTTTATCACAAGTCAAGTGCTGAAATCCCTGGGCCCCTGCTCAAATGCCACCTCTTCCTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAAGAGCCATCCCTGCCCCTTTCTTTGCT
EST16100 1	24	C	G	ATCCCAGCTGTGAAGGACGCAGAGGAG[C/G]GTAAACACAGTCCATTTATTATAAGGGGTGTGCACATTCCAGGGGCTCCAAATAATGCAACATTGTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC
EST16104 9a	83	A	G	TTCTTTTAAATAACCCAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAAGTGATTTGCAGCTGGTTCCTCCAGGGA[A/G]TTGGCCCGAAGCTGGCTCCAGGACCTCAGTC
EST16118 0b	119	T	C	ATGGTATAAACAAATCAGTTCCAGGTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGCATGCTCCTAAAACAACTAAAACAACCCTCTACGTGTAATCAGTCACCTAAGATATCGAGTGGCAAGTCTTTCACA
EST16118 0a	32	C	G	ATGGTATAAACAAATCAGTTCCAGGTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGCATGCTCCTAAAACAACTAAAACAACCCTCTACGTGTAATCAGTCACCTAAGATATCGAGTGGCAAGTCTTTCACA

ID	Pos			Short seq		Sequence
EST16151 2	53	C	T		...	AGCCAATTCAAACGAACTCTATCAAAAACACACAAAGGCCTAGAGGAGGAGATTA[C/T]AATGAACGT AAATAATTCAAGGCAATTTTGATCTAAAGCATTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTTGTATAGGA
EST16182 6	54	G	A		...	CATTGGTTGGGTAGGGAAAGATAGTAGTGTGCAAATAAAACACGACAG[G/A]AAATGGAA TTATAGCTTTCTTTCATATAGGGAATTGAAATTTATTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59	A	G		...	GCAGGTAAACTGTGGTTCACAACGTATTGTTCTTCATAAAGAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGTCTGTCCTGGCCCTTCTCATATTTTATGTCACTGTCCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28	G	A		...	AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTCGCATTT CCCCAGAGGAGGAAAAAGTCAGCATCATAAACCACATGGGTCACATGCTCACGCACATGGTGTC
EST16229 2c	52	T	C		...	TGTGAACTCGAATTCGCTTGTCCAAGTCCTGAGTCACAGTTTCATTGGGAG[T/C]CCCTGTGCAGCC CTTGCCAGTTCCAGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGGAGGCTGCA
EST16229 2b	45	T	C	GGAGCCATTGT TGGGGTTA G GTTCAGGACAG	...	TGTGAACTCGAATTCGCTTGTCCAAGTCCTGAGTCACAGTTTCAT[T/C]TGGGAGTCCCTGTGCAGCC CTTGCCAGTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGGAGGCTGCA CAGACTTTTCCTCACACCTCATTGGCTGGAACTGGGTCACACATCCTTGAACTATCATTGGCAA AGGGAAATGGGTCATCAAAATTGCTTAAGGCCAAGCAGGAGGCCATTGTTGGGGTTA[A/G]ACTGTCC
WI-16816	124	A	G			TGAACAAAATCTAGGCTC
EST16269 5b	49	G	A		...	GCCACTCTCCTGTGTGGCTTGCTCCTGTCCAGCTGCTGCCCAGTGCCACA[G/A]TGGTCTAGCCTCCATGG CAGAAGCATTTTAGCCAACTGCCAACTCCTGGTGCTGCTCCCACTCTCCTTCCTCGCCGGGCTCCACCACC TCTTCCTCCTCAATC
WI-16824b	83	G	A		...	GTCACCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGTG[G/A]CTTACACCTTTAGCACGGATAGTTCCTGGTCCCAAGTGGGTGTGGA AAGCTGATAAACGTGG GCCTTCCATTATGGGAATA
WI-16824a	47	T	C	TGATGGTGCTG TTCTTCATAAG CAGCTGT		GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGT[T/C]GTTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCCTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96	T	C		...	TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAACT[T/C]GGAATAAGAGCATAAAAACGGAACAGTAACATCA
WI-16857	47	G	A	A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AGACCACT	TATAATCCATCCTCCAACACACACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAATTGTTTCCTGATAATGTGGGAGAAATCTGCTCTTTATGTA

Marker	Pos	Allele 1	Allele 2	Sequence 1	Sequence 2	Sequence 3	Sequence 4
WI-16879	79	C	T	GATACAGGCC ATATTTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG	GCCATATTTCCCA[C/T]ATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAACAGGCACCCAG
WI-16882	99	A	G	GAAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAAGACAATTCTCCCCCTTCACCCAAAGGTTACTCTGAC	AAGGCTATGAATGAAAATGCCACGTCTCTGAC[A/G]GCGATTACCTGACATGTGTCATCTCCCT
WI-16888	70	G	A	GCTAACTTTGG GCAGGTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTCATCACTACCCGGGGAGAGCAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG	TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C	T	ACTTGGCCTGT GTTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTTGTTGTTATTTGCCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACTTGGCCTGTG	TTGTTCA[C/T]CCCACTGCCTAGAGAGTATAGACA
WI-16910	74	G	A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAGAGTAAAGATGGCG	CTAGAA[G/A]GTATCTGTTATAGAAACGATACTTCATTTGGGCCTGAACCAGTGAAGGT
WI-16918	93	C	T	CAGCCATTAA CCACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATTCTCTCTGCTACCACAGAGCACTAAAATCTAGGAATTTGAC	TTTACTGCAGCCATTAACACCAGCAC[C/T]GATGCCACTCTTCTGTATCAGGAACTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127	A	C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTGTAGAGGTCTCATGGAAATAGGCCTGGAGCACAGGATT	TGGCTGAGGCTTTCAACTGACATCGACATCAAGGAAAGCGAATCAAGGGAAGCAGACCTGGGG[A/C]CCA CGGGCAATCACATGAGATG
WI-16947a	58	C	G	CATGGAAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTGAGGGTCTCATGGAAATAGGCCTGGAG[C/G]ACAGG	ATTTGGCTGAGGCTTTCAACTGACATCGACATCAAGGAAAGCGAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43	T	C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTTACTTAAAATGCACACTACATAACAACCTAATA[T/C]CTTAACTTGGTCCAACTATTT	AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAAA
WI-16995	55	T	C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCCGGT	TTGAGTGCCAGACATCAAGCATAGAAAGAGCAGTAGAGACTGAGGTAAATAGTATT[T/C]ACGGCTGG	AAATCAACACATGCCTCTTCTTCTGTGAAGTTGTCAGCATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60	T	G	---	CACATTCCCTT ACAGTCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAGTACACTGT[G/A]CCCTCATCTGAGAGTGTG	TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA
WI-16992a	46	G	A	AAGCACCCAG AAGTACACTG	ATC	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAGTACACTGTC[G/A]CCCTCATCTGAGAGTGTG	TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA

ID	Pos			Flank 1	Flank 2	Sequence
WI-17010	23	T	C	TTCAACAGGAAAAGCCATG	AATAATACGGTGTTTGAATGTCA	ATGTTTCAACAGAGAAAAGCCATG[T/C]ATGACATTCAAAAACACCGTATTATTAGAAGCTCATTAATTGTTTAATGCAGACAAAAATCAAGGTCTAACTAAAGCAGATCCAGTAACTAAGTGATCAACCTAGAGGTTCCCACG
EST171279b	74	C	T	CACTCGGCACAGACAGAGT	GGGAGGGCCAGGGGTG	ATTCCGTCTCCAAACAGCATCCCAGGCCGGCCATCTCCCCCAGCGATTTTATAATACACTCGGCACAGACAGAGT[C/T]TGGGAGGCCATGGGGCACCCTGCCCTCCCAGGCTTCCTAAGTAACAACT
WI-17040	94	T	C	AATTCTCTTATCATCTCAAGCCA	GGACTATGGCTTATTCAGTGATG	CACGCGTTCATTAAATTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTCGAGAATTCTCTTATCATCTCAAGCCAGT[T/C]CATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTCCAAATCTTTCTCATATTGT
WI-17044	47	G	T	GCCAGGGATTAACGTATAGG	GGGGATCCCCTTGTTTAAGA	TTGTTTTGTTTGTTTCTCTCCTGCCAAGGGATTAACGTATAGG[G/T]TCTTAAACAAGGGGATCCCCACTTATAGTCGACAGCAGCAGCTCCTGCGAATGGCAGGAATCGAATCAAAAGAAAAGCAAGTG
WI-17021	62	T	A	TGGACTTGTCAGCCTATAACTACTC	TGTAGAGTTAGTGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTGCAGCCTATAACTACTCT[T/A]GCAGCTGCCACTAACTCACAGGCACAGTAACTACACTTTATACAGGAGCACATGCCAAAGTGCCTGGGAGGTGCCAATAAAATCAA
WI-17065	90	T	C	CCAGAAAGGAAAAGCATAAACTT	CCCAAGAGACAATGAAATCCT	TGTAAAAAATGTAGACACATGGGGGAAAAAACATTCGTAATCAACATGTGCTGTTTCTACTTCCGGTACCAGAAAGGAAAAGCATAAACTT[T/C]AGGATTTCATTGTCTCTTGGGT
WI-17066	32	A	C	TGTACAGCCAACATCACTGTTCT	GAGATGTTGAAAATGTTCTGGAA	TTCATAAGGTTGTACAGCCAACATCACTGTT[A/C]ATTCCAGAAACATTTCAACACATCTCAAAAAGAAACTCTGCACCCATTAGCAGTGTCATTCCCTGTAGCTTCCCTCATAGCAATGGCAACTGCTGATC
WI-17074	86	T	G	⋯	⋯	TGCTGACTGTCATGACTTAGTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCATAACCTCCTACACAGGCCTTT[T/G]CTACATAGGAGTATATTTGGCCAAGACTCACCACTAGAAGTGATT
WI-17104b	108	T	C	⋯	⋯	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCCTGATGCTTGCGAGCTTCCCATTCATTCCAAATCAGAAGCAGTCAGTCAGTGGCCCCGTGGTTCCAGACGGC[T/C]CTCTTTGTTAAGAAATTA
WI-17114a	37	T	C	TTTCCATCAAGGACTTGTTT	TTGTATTATAAATAGCAGAGTGAAGAGAC	AGCGTCCAACAGAGTTTCCATCAAGGACTTGTTT[T/C]GTCTCTTCTTCACTCTGCTATTTATAATACATAGCAGAGTGAAGCTACCTCCCAAGGCCAGATGCTCTAAAGTGCTAAAAGAAGACTGCAGCCACAATCAGAGTTACATGGGA
WI-17150	76	T	G	GATGAAATTCAGATAGTCTTCGCTCTT	TTCTCAGAATCCTGGAAGATATG	CGTGGCTGGACTAAGTCGTCTCTTCCATGTGGACACATCCCACTGAACAGGATGAAATTCAGATAGTCTTCCTCTT[T/G]CATATCTTCCAGGATTCTGAGAAGGGCCTCCTTGTTGTGTCTCTAATTT
WI-17163	43	A	G	CATTTCTTTGTAAAATAACAATAACGTT	CAGAATCTTGCTTTTGCCTT	GAAATCGAAATACGTCCATTTCTTTGTAAAATAACAATAACGTT[A/G]AAGGCAAAAGCAAGATTCTGTAAACCAACATTGGAAAAGGGGACACAGGAGGGGGAAAGGGCCAGATTTTCAACGGTTTCCTCCACATCTGCAGACAAA

ID	Pos					Sequence
WI-17178	127	T	C	GGACTCCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAAATGTCCCCTCCAATTCATTCATTAGCTATGATGAGGAGTTATCAGTTCATTCATTTCAGAGAGCGAATTACTGG GGCGGAGGGGGTTTAATATCCTGATGGGTTAATTCAGTGAGGACTCCCTCATGAGGAGC[T/C]AGAA GCAGTTGAAAATTGAGGG
WI-17180b	81	C	G	...	...	TCATGGACATCCTGAAGCAGCAGACACAAAAATATAGAGAATCCTGCACTTCCCAAGTCTCGTCGCACAG GCTTCAACAATTAC[C/G]AACATCTTGCCCATTTTGTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17180a	47	T	C	CACAAAAAATA TAGAGAATCC	TGCGACGAGAC TTGCG	TCATGGACATCCTGAAGCAGCAGACAAAAATATAGAGAATCCTGCCCATTTTGTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17156	54	G	C	TGTTCTCTAAA CTTTAGATATC TGTGGAA	CAAGAAATAT ATATTTGATTC	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCAT[G/C]TTCCACAGA ATCAAAATATATTTCTTGGTTGGAAATTTAAATGTTCTTAACTATGTTCTTAACTATCTGCCTACCACCACCTCAAT TAATATTCTTG
WI-17149b	79	T	C	...	...	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCAGCGTGCGTGGAA ACCCAATTGTCAT[T/C]GTGTATGAACTACAAAAGGATGGGAAAAGAACACATTTCCTCACA
WI-17149a	48	C	G	CAAGGTTTGA AGGAGGAACA	CCACGCACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACAT[C/G]TCATGCACGTGCGTG GAAACCCAATTGTCATGTGTATGTGTCATGTGTATGAACTACAAAAGGATGGGAAAAGAACACATTTCCTCACA
WI-17197	67	G	A	GCAGAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAGTAGCTGGGGCTAC[G /A]GGTATGCACCACCCTGTTTAATAGAATATTGACTTTAGATGCGCA
WI-17198	38	A	C	TCCCCCCTTGTC CCTAGTTT	TCCATTTGTCC ACTGAGAAATT	TGTATTTCAGTACTTTCCTCCCCCTTGTCCCTAGTTT[A/C]TAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATCAGAAGATATCTTACAGAGAACAATGCACATCC TTC
EST187538	27	C	T	CTACCCAGGCT GGTCTCAT	GGATCGCGATGA GCCTGA	TCGCTATGCTACCCAGGCTGGTCTCTCAT[C/T]TCAGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG GATAAGACACAACTGCCACCAGGCCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
WI-17108b	74	C	T	GCCATTCAGTC TCAAAGTAAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTAAAACATAACCAGATGCACCTTGGTTTTTACATTCTCTGGTTGCCATTCAGTCTCAAAGT AAACAC[C/T]TGGGAGCATATGATAAATCGTAGTTTAAGGAAGCCATAGCACTTACAGAGT
EST190672b	41	A	G	...	...	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA[A/G]GTGGCATTAAGTACATTCAACT TTTTGAGCAACCGCCATCCATCACCATTCATCCATCCATCCGTT
EST190672a	40	A	C	CGTGACCATTT AAGGGTATAG TTC	AAAAGTTGAA TGTACTTAATG CCA	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTC[A/C]AGTGGCATTAAGTACATTCAACT TTTTGAGCAACCGCCATCCATCACCATTCATCCATCCATCCGTT
EST191258	28	A	G	...	...	CTGTTTCTCAGAGATGACACTGCCAACA[A/G]TCACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAATTTACAGTAGTGTTTTTCCTGAAAA

EST					Sequence
EST208248	115	T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA ATCTTAGG	GTGTGGGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGT[T/G]TCGGGTCCAAGATAAA
WI-17347	50	A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCCAGATGGGGTCACATCCTCTCAGAACTTCTCAGCCT[A/G]TGTAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGGGATGTGAGTGGGGACCA
EST219047b	128	G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTC AGAAAGCAT	TGATTGTGGGTCTGGGAGCAGTGGGCAGTTCAGTGAGGAGCAGAGGAAGTAGAGCCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAATGTACTAGGCTTTCATATGGCCATTTTAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST221113	82	T C	GAAGATCTGT CTGGCATTCTT T	TGGAAAAACA GCCCCAC	CAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT CTGTCTGGCATTCTTT[T/C]GTGGGGGCTGTTTTCCAAGGCACA
EST221972	78	T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTAATGATCACTCACCAAAATCCACAGGAGAATCTTAAATGTTACAAGCACCAATTATTCTGCT ATTCCTGCCATT[T/C]ACCGGCATCCTTCATGGTGAGTATCACAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST223119c	92	T C	...	...	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAATCCACCACTGTAAACAG TAGCATTCAATGGTTTTTACTCTA[T/C]TGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATTCATTCCAG
EST223119b	54	A G	...	...	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAATCC[A/G]CCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATTCATTCCAG
EST223119a	41	T C	GGATTAGATC ATCTTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATAT[T/C]ACATAAAAATCCACCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATTCATCCAG
EST223197	19	A C	...	...	TCGAGGAGCTCTGAGGAGC[A/C]CACCAAGGAGACGTGTGTCCCAGGGCCACGGTGCGAGGCAAGTGTG GTCCAACTCCTTCCTCCCCTTTACAAAACTCCAGCTCTGACAGGCCTTCT TAAGCCTTTTTTAACTGT
EST224333c	103	A G	AAGACATGTT CACCAAGTGA AA	CAGCTTCAGCT TAACTGACAGA G	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCCAGTGTACACATGGAAAAGACATGTT CACCAAGTGAAACCAATCTAACCAGAAAAGCTTTACC[A/G]TCTGTCAGTTAAGCTGAAGCTGAAATT CTGGGAGCTTGACATGCTG
EST226579	71	A G	AAATGGATCC GCATGAATTTT T	AGTTTCAGTTT	TATCCATTTCAAGAAAAAAAAAATGACTTAAAAAATACAATTCTATCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAAAAAATTCATGCAAACTGAAACTATGCTTT

ID							Sequence
EST22993 5b	71	T	C	TCTACCCCC	ATCCTTTGTT	TTTGACTGTAA TTGCCTGTTAA	GCTTTTATTGTCTCCTTTAACATCAAATGTTTATAACACACTGATCCTTTGTTCTACCCCA ATT[T/C]CATTACAGTCAAATTAACAGGCAATATAATAGGTCTAACAGAATGCTTGCATT
EST23021 0	108	T	A	---	---	---	TTATTTCTCAGCTTACCATTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTATTAATCTTTGCCTT[T/A]ATGGTTTGACAGTTTGTGTCTTTCT T
WI-17387	55	C	G	TGAAGAAAAA	CCTTTGCAGAT	AGATTAATAGT AACTACT GCTTTTGCCTA	ACAGAATTTAACATGCAAGTTCATTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAATCTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101	A	C	CCAGAGGCAG	AATGTAAGCT	CCTTCCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAATAGATGAAAAGAGAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAAGCTCCAGAGGCAG[A/C]GCTTACAGGAGGGGAAGGGACGGCTGAGGC CAAGAGTGCTGGCTCACTG
EST23733 9	31	T	G	TT	TTGTTTTGTT	GGCTGTTAGTT TGCACTTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTGTTTGTTTGTTTTTCCT[T/G]TATTGATGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCCTAGAGAAAGATATGAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83	A	G	CCAG	GTCCCGTCCCG	CCAGTGACGAG GCCGA	CTGACACGTCCCGTGTGTGCGGGGGTGTCCATGTGGCGGTGTGTGAGTGAGACTTTTACTGCGTCCC GTCCCGGCCAGCCCT[A/G]TCGGCCGCCTCGTCCGTCGGCCGTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTCC
WI-17519	55	T	C	A	TGCAGGCAATA	GTTGTCCTAGC TAATGAATGC AATTATTATT	TTTTTAACGAAATCTCACTACTGCAAATGCATTGTTGTCCTAGCTAATGAATGCA[T/C]AGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAGAAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95	C	G	---	---	---	TCTTTGATACAGGTAACCAGTTTGTAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAAGTCAACATCAGGATTTCTTTT
EST25356 3a	26	A	C	---	---	---	TCTTTGATACAGGTAACCAGTTTGTA[A/C]ACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAAGTCAACATCAGGATTTCTTTT
WI-17581c	99	C	T	---	---	---	GGGTGACGGCTCCAGAATGGGAGACAAGCCAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAATGATAGAACCCAA[C/T]TAGGCGCAATTTACATTGACGGCGTCATGC
WI-17581b	86	T	C	ATTTGATAA	ATTCAACATT ACTACCAGTT	CGTCAATGTAA ATTGCGCCT	GGGTGACGGCTCCAGAATGGGAGACAAGCCAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAA[T/C]GATAGAACCCAACTAGGCGCAATTTACATTGACGGCGTCATGC
WI-17596	86	A	G C	ACTTCCTTGTG TAAACACTCC CAATAT	CATTCTTATAG CTAGAAATCGA		GTGTGCTGGTAAATGGATAATAAGCAGTCTCTCATCTCTGAAGGGTGGAAGTAGGAGAAAGGCCTACT TCCTTGTGTAAACACTCCC[A/G]TATTGTCGATTTCTAGCTATAAGAATGGGGCCACTAAGTGGGTC

Clone	Pos	1	2	Fragment A	Fragment B	Sequence
WI-17623	46	T	C		...	TGTGGTTTAATTTAATTCCCATATAATTAATTAATGGTGGCACATT[T/C]GCATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAATCTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b	46	T	C		...	ATTTCATACAGAGATACAAAGGCACAACTATGTGCAGCAACAATCTGA[T/C]GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTAAATGTCATGGCTGGTTCGGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35	C	A	ATACAAAGGC AACTATGTGC AG	CAAGAAGTTTG GACTGCCC AG	ATTTCATACAGAGATACAAAGGCAACTATGTGCAG[C/A]AACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTAAATGTCATGGCTGGTTCGGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69	G	C			TCAGCTTTAATTTAAGGGACATGTAAATAAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG[G/C]AGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCTCGTTTCCATCTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39	A	G		...	TACTTCAGTTTAAGGCAAATTCCACACAGAGACTGTCTC[A/G]GAGACGGGCACAGAACCAGACACC GTAGAAACACCACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101	C	T		...	CAAAGGATTTTATTTGTTCCCTAAAAAGTAAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAAACATTTCAATCATTCTCTCTTC[C/T]TTCACATGGTGTACTCTTCATGTACACAT CATCGGAAAACAGACTGA
EST27504 0a	33	G	A	GCACTTTGCAA CAATTTAATA ATTT	GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACTTGCAACAACAATTTAATAATTTATC[G/A]CATTACAGTAGTAGCATCACACCAGCAGTCAAT AATGCCACTTAGGCAAAGTCTTTCAGTATTTCTGTTACCACATTCTGTTAACAAGAACCCATACATT GGTAAAATTCATTCT
EST27662 4	51	C	T	CACATTCTGTT CTCCCAGTCTTG C	GCTTATGTAAC C	AICTTAAAGGACCATTAGAAAAGGCCAGTCACATTCTGTTCTCCCAGTCTTG[C/T]AGGTTACATAAG CCATTTCCATAAATTCTATAGCCTCTTAGAGTAACACACTCTTGTTTGGAATGTTC
EST27788 3	100	A	G		TTATGGAAATG ...	ATTTTATTAGGCGGTACAATTCCAAGGTGGTAAGGGTGAAAGGAAAGGCGAAGGCAAATACAT TATTGAGCTGAAAACAACTTTACATTCAAGGAC[A/G]GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58	G	A	GGAAGTCATC AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAAACTTTCCTTCTGTTGGATCCCAGTGACGTGGAAGTCATCAGAACCCAC[G/A]GTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTCTGCTCAGTCAGTCACAATTTACTTGAA
WI-18369	58	G	A	AATAAATTTC AATCTGTCAC ACAATC	TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTCCCCAATGTAAACAATAAATTTCAATCTGTCACACAATC[G/A]AAATG GATAAAGGCCTTCTTGACAAATTTCTGCCACCTCCGTTTAACGCATCCAGAAGTCAGAACTCAATCTTATCTC
EST28036 4	37	T	C		...	TCCCGCTTCCAAAAGCTTTATTGGCAAATCATATGCTCTA[T/C]AAAAGAATGATCAATCCTGTTGCCTCT AAGTCAATGGAATGAAGAGAGCTGTGTCCAGGACACCACGCCGTGCTGAAGGAGACTGCTGTGTGTG TCCACCTCTTATTCATAG

ID	Pos					Sequence
EST284837	31	T	A	GGAGTAAAAG GTGTTTCTTCT TTAAA	TTTCTCGCATT TATTTTTATAC CA	CATTGGAGTAAAAGGTGTTTCTTCTTTAAA[T/A]ATGGTATAAAAATAAATGCGAGAAACATTAAC GGAGAATGTACAGACAACAGACGAGAGACATAGTTGTTTCTGACTGTGACACATTGGTGAAA
WI-17724	50	T	C	TGGGCCCTCCC TGTC	TGGGTTGGCAG TGTCC	AGAATTGGTCTAGTAATCGTTCAGGATTCGGTGATGGGCCCTCCCTGTC[T/C]GGACACTGCCAACC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68	T	C	...	...	TGAGCCTGGGGAGAAAGACCACAGAAGTGAAGTGCTATTAGTTACATCATCACCAAGTGTACATACTG TTT[T/C]CACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTAGTAGTGTGTCA
WI-17730a	39	A	C	GACCACAGAA GTGAAGTGCT CATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACCACAGAAGTGAAGTGCTATT[A/C]GTTACATCATCACCAAGTGTACATA CTGTTCACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTAGTAGTGTGTCA
EST290415b	53	G	A	GGAACAAACA CATTAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAAACACATTAAGCATCATTGTCACT[G/A]GCTAACTCCT CAAATCAACAATACCCTTTATTTTTAGCCATGAAAAC
EST291284	58	A	G	...	...	CTTTTAGAAGGACACCAGTCTTGTTGGACTTAGGCCTACCCTATCCAGCAGGTGCC[A/G]TTATTT TCACTTGGTTACGTCTGTGTAAGGACCGTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTTGCTGGGGACACT
EST299123	103	C	T	TCTGCCAGCTT TCATTCTTCTG ACAGGCT	GCGTAAGTGTC T	ATTTATTAGGTATCTGCGTGTTGGGGGTGGGGGTGGGGGAGATTGTTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAAACATTTCTGCCAGCTT[C/T]ACAGGCTACAGAAGAATGAGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST299368	121	G	C	...	...	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAAGTTAACTCACCATGAAA TTTAACCTTCTGTTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCCTG
EST302232	99	A	G	...	...	AATAAAATACATCATGGGGAATGGGATATCCATCCCCTCAAGCATTATTCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTAATATTCC[A/G]GGATTTAATTCTTCCTAGTTCAATCTCTGGGA GG
WI-16260b	86	G	A	...	...	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTCACAATATAGGTAGC[G/A]ATAACCAGGTCTCACTTCCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59	G	T	TGAGGTGGATT CAAGAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTGTGAGGTGGATTCAAGAAGAAAAA[G/T]ACCC AGAGTTTCACAATATAGGTAGCGATAACCAGGTCTCACTTCCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30	G	A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAAACAGGAAATATTGTGCTTTCTTG[G/A]GCCTGTTCTATAATGTTCAGCTTCAAATTCTTTG CTTATAAATCCAATCAAATGAATTACCTGAATT TTCTCCTCTGTTCAAAA

Clone	Pos	Allele 1	Allele 2	Flanking fragments	Sequence
EST31951 4	87	C	T	GGGTTGTCCAG CCCACCAAAAT CCAACA CACCTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTCACTCTTTAGCAATGACA TCGGGTGTCCAGCCACCAACA[C/T]GGAGGTGATTTGGTGGGGAATTCTTATCACAATTATTCT
EST31968 8b	95	T	G	...	CGAATTGTCTCTCTTATTTGTGATTCTAGTAATCCTAAAAGATTGGGGGGCGGGTTACTATAAGT GCATTTTATAAATGGGGATTTTCTGCT[T/G]AACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T	C	GCGGGTTACTA TAAGTGCATTT TGTAAGAATCA GTGGGCAGTT T	CGAATTGTCTCTCTTATTTGTGATTCTAGTAATCCTAAAAGATTGGGGGGCGGGTTACTATAAGT GCATTTT[T/C]ATAATGGGGATTTTCTGCTTAACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C	T	...	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCCTTCCAGACCTGGCTTTGTAGTT[C/T]GTTCAGGCCCATTGAAAATAGCAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A	G	...	AAGGCTTCCAAGCATTCAAAGGCACTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCC[A/G] [TCTGTATTAGGGAGCACCCCAAGCCCCAGTAACAACATATGGTTCTTGCAG
WI-17800	29	C	G	GGGAGCACAA GAGAAACTCA TTTCCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAGAGAGAAACTCACT[C/G]AAGACTGGGATTAATTGTAGGAAATATTTCACAG TTTCCACAAGTCAGAGAGAGCTAATCCCAACCCTCGTATCTGGAACATACACTGCTGCCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T	G	CCTAAAGTCTG GGATGACTTTC CCGGTGTCACT TCTACTTGATG C	AAACTGTCATTCCTAAAGTCTGGGATGACTTTCCT[T/G]ATTCTACATCAAGTAGAACCTAAGCCAAT TCAGAATCAGAATCCTTTTGTCCATCAAATTCCAGCTAACTCCAAGCTGAATTAAATGTTCATTCT
WI-17860	121	T	A	TTTGCCAGCAA ACTAAGGAGC AGTCAGTGG AGCAAATA	GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAAATCTTTA TAGTGTCCAAAGATAATTAATTCTTGGTTTAAATCTTTGCCAGCAAAGCAAATA[T/A]CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A	T	TTTTATAGCCT ACTTCTCAAA ATTGTT CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTTTGTTTTATAGCCTACTTCTCAAAATTGTT[A/T]TTTGTGTGATTAGTGACAACG GGGGAATCTACACTCACATGCTCACATCAGTAAACTACCA
EST33301 4c	80	G	A	...	GAAAAAAAGTCAAATGTGTTCCCTTATGGGTGATGCCACCATGCCTCCACACAAGCATGATC AATCGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G	A	...	GAAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCAT[G/A] ATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G	A	AGGCTGGTTTT CAATACTAAA CA CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAGCGTGGTTTCAATACTAAACA[G/A][A]TGTAAACAATGCAAATATT TAACAATAAATACACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTGCAA

Marker	Position	Allele 1	Allele 2	Flank A	Flank B	Sequence
WI-17904	50	A	G	AAAGCATGAC AATAAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAAATGAACAC[A/G]TACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAAATGCAGTAAAACAACAACAAATGA
EST341495	69	A	G	GAT	AACTACTAGCG CG	GTTTTTCTTGAGTGACACAAGCTGTTCATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTTGGTATTCTATGAAAAAAGCAGCTAGTTCAGC TTACAAATCACACAAGT
EST343438	95	C	A	...	...	TGGGAAAACATAAGTTAACTCAAGAATATATTCCAGTCTTTATGTTGTTACTAAAACATTGTAATAGTGT TTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAAACTTACCATCAAACACTTC CAGTGCATCAA
WI-17982	98	C	T	GGACCATATG ATATATAACT CCTTCC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTTAATGGAAGGAACCACCACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCCTAAAAGC[C/T]GGAAGGAGTTATTATCACATAAATTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118	A	C	...	...	CTCAGTAACTCCGGTGTATAAATCTGCCATTTATTGATTTATTTATGATAAAACAACCTCTCATTGTGA AAAACAGCTAAGGTGACATCTCCAGACCCAACCACTGTCCCTGTAATGT[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84	A	G	GTAGAGGCGA AGGGAACAG CAGC	AGGCACATGGG CAGC	CCCATCCAGAAACCCCAGTGTGATGGTGGAAGCAGCATGAAAAÍCAACATCTCCCAGGCCTCGCCAGT AGAGGGCGAAGGGAACAG[A/G]GCTGCCCATGTGCTGTCTCTAAAGACGGCCACCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33	C	G	...	...	ATTCTTTATAAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041	24	A	C	...	...	GCCACTGAAAAAAGGTGCTCTTCC[A/C]GTTCTAACTCCCTGGACTCCCTCATTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTGCTGTATTTAAAAGGCAGTGTTGATGCTCCAGGAT TCAAATACTTAATCA
EST351648a	57	A	G	CACAGCCCTGC CCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCTTCAAGCACAGCCCTGCCCCC[A/G]TCTTGA GATTCAGAATCCAGAGGGTGCTCAGTCCTTGGTTAGGTGCTTCGTGTGACATTCCTCTG
WI-18052b	67	A	G	...	...	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTCATGTACGAATCTTTGGTTACACATCTTAG[A/G]ACAGCAGAGCTGCCTGAGGGAGGAGGGTTGTGTTTAATGTCGTATGCATGCTCAGCACAGTGCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50	T	C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTCATGTACGAATCT[T/C]TGGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGTTGTGTTTAATGTCGTATGCATGCTCAGCACAGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46	G	A	GGGAGGTGGGG GAGTAAAA	CGTCACCCTGC TTCCA	CTGTTGTGCTGAGAACGAAGGAGTCCAGAATTGATTTTGTTGGTTACACATCTTAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAA[G/A]TGGAAGCAGAGGGTGACG CATGCAGGAGTCCAGAGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

Marker	Pos	Allele 1	Allele 2	Left flank	Right flank	Consensus sequence
WI-18064	54	G	A	AGA GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAACCCTGTGGGTAGCTGCTAAGCTGTATTCAGA[G/A]GAATGTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGGCTTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T	C	GCATAAAATT TTCCAGTTGGT AA	CCCTCGGCACC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGGTGGAATTTTGTGTATCTGGCTTCAT GGGATGCATAAAAATTTTTCCAGTTGGTAAG[T/C]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	A	C	AACCCACTAC TTACTCAGAGT GTGTAT	AAAACTAATA AGAAACTGGA GGTTTTT	AAACCCACTACTTACTCAGAGTGTGTAT[A/C]ATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTTCTTATTAGTTTTGATATTTCTGTACTCAGAAGCATTTAGGTTGCAAAGGATATAA
WI-18080c	80	C	T	---		TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTGTAATTAAAATCTACTATGCCGTG TTTGACTTTTAT[C/T]CTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18080b	65	G	A	---	---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTGTAATTAAAATCTACTATGCC[G/ A]TGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18080a	41	T	C	GCAAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCT[T/C]TTGTAATTAAAATCTACTATGC CGTGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18086	63	G	A	---	---	GTGGGCATCCTATAAAAGCAGCCATGTGTTGAAACAAATGATATGCACAGAAAAGCATACTTCT[G/A] TGGCTTTGTTGTTACACGGGTTTCTTTCAAGAGGAAGATGACTCAGCCTCCCAGCTCTGCAGTCTAGC TTAGGAGAGGTGTTTGAA
WI-18115b	71	C	T	---	---	AACTACACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATTCCC TTC[C/T]TTTGGTATGGAAAGACACCTCTGCTGGAGGACTCATTACACATGTAAAGAAAGGGGTGAG TCAGT
WI-18115a	70	C	T	TTAGTGTACCT TGGTATTCCC TT	AGAGGTCTGTC TTTCATACCAA A	AACTACACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATTCCC TT[C/T]CTTTGGTATGGAAAGACACCTCTGCTGGAGGACTCATTACACATGTAAAGAAAGGGGTGAG TCAGT
WI-18136	78	A	G	---		TTTTGAGAAGCACTCTGTAAGGCAAGGATGCATTCAAAAAAATGGCTTTGAGGATTAATCTCTCTTTA GGTAATTTGC[A/G]TAAGAACAATAAAAGCATTTTAAAAGTCCACTGCCGCCTTAGAAACT
WI-18169	115	A	G	CCATCTTCCG GAAGCTC GTGCTCCA		GGCAAAATATTTTTACATCACACCTGGAATCTGCCCAAGTCTTTCCACTGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTATCCAAGCAGCCATCTTTCCGGAAGCTC[A/G]TGGAGCACAAGCAGA ACTCGGGTGGTGAGGTGGA
WI-18190b	26	G	A	---		TGAAAGAAGTCGACACAGCGGACACT[G/A]TCATAAGTGGAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATCAAGAGCTGGAGACATTAATCCTGGCGA

ID	No.					Sequence
WI-18190	62	G	A		...	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAACAAAGGATGAAGCTAATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGAGGGACAAAATCAAGAATCAAGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100	A	C	AAATATATAC AACACTCCCTT CAGATC	CGTTTTACCAT TTGTTAAGCTT TTG	GACAGTGAAAACATTGAAAAACACAACAAAATGTAAATCCAA TGTGTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAACGTA TGTGTTCTTGAAC
WI-18215	78	G	A	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT CCCCC	ATTCATACAAGCATTCCTGAGTACAAACTAGGGACACAGGTATTTCACAAAACAAATAGAGCAGA GTTCCTGCCCTC[G/A]GTGTGCGGGGGGGAGAGAGGGGATTCAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60	T	A	TGGTGTTGATT GTGATACACTT AA	AAATAAAGGT TTTCAGGGGTT C	CATTTCCGAAAATCTGATAGTTAAAATATCCCGTCTGGTGTTGATTGTGATACACTTAAG[T/A]GAA CCCCTGAAAACCTTTATTTGAAATTGAAGTTTTTGCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76	T	C	GGAAAACTTG AGTTTGAGATC ACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTCCTCAGTATTTATCAATAGTGTGTAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]C[T/C]GTCTCCACTAGTCTATTCACTCTGTGGGCATTTCGGCAGAAGTGGC
WI-18242	30	G	A	CCCCAAATGTT TACTGTAACAG AATCGTAACA	GCTAACACTTC CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTTAGCAAAAT TGGATGCCACAACTATCTCACCATTCCTTCAAGCAAGTGAGGGTCAGAATGTTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119	C	T	...		GCATCAGAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T	C	...		GCATCAGAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]GAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C	T	AAATAGGAAA TATGGACTATC TTCAAA	TTCATGCATCA TTTGTGCA	GCATCAGAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAATATGGACTATCTTCAAA[C/T]TGCACAAATGATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A	G	GCTGTCAGCTA TTGTTATTTCA AA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTTGGATATGTGGTTTAGTGTCTATCATTAATTTGGAAAGCTGTCAGCTATTGTTATTTC AAA[A/G]TATCTTCTGCTCCCTTTCTCCTTTTCTGGGATTCTCATTCTGCATGTGTTATA
WI-18330b	66	A	G	...		AAACATCTCACAGCTGTCTTAGGCCATCCTGTAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAAGAACATAAATTTTTGTTGAT TCACA

Clone	Pos.	Allele 1	Allele 2	Flanking sequences	Sequence context
WI-18330a	49	G	A	AAGA / TCCTGTAAGA AATCAGGGAT / AGTCCTGACTC ACTGCCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTGTAAGAAAAATCAGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTGCAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTGTTGAT TCACA
EST37564 5	85	T	C	AGA / AAATTCAAGC CATCTACAAA / CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAGAT[T/C]TCTCATTGAGGCCTCCATAGGCTGCAAACACATCAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G	A	TT / AAACAGCTTT CGTTAGGCTAG / CGCATACAATG GCTCAGC	CAAAGGGATTTATTACCTACAACAGTAAGGAGGACAGCTGGGCAGTTTCCCAAAGCAGTACCTC CCAAAACAATGGTGAAAACAGCTTTCGTTAGGCTAGTT[G/A]CTGAGCCATTGTATGGGAGGCAGA GT
EST37624 6b	102	G	A	---	GTGGCAAGAGCAGCTAAAACACACTCATTTGCATGAACTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCCTCCTGCGTGCTGCTTGGCTCTCTGGACG[G/A]TCATTCTACATGGCTGCTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C	T	---	GTGGCAAGAGCAGCTAAAACACACTCATTTTGCATGAACTCCAAATACGAACAGTGCA[C/T]GCTGA TGGCCTGCAGTCCTCCTGCGTGCTCTCTGGACGCGTTCATTCTACATGGCTGCTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C	G	AAGGACTCAA / CCCAGCCCTTA GCATCAA / GA	AATGTTTTAAAAAGTCCTACCGTGCTGAGGTGGCCATGAAGCCAAGCCCATGGAGAGACATTTCAGA TAATCCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTGAGTCCTTCCAGCCCAGGTCCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A	G	---	TTTTATCTGGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTCGTGA[A/G]GTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G	A	---	TTTTATCTGGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C	T	GCCACTTTGC CCCTT / TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTT[C/T]GTGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T	C	---	TTTTATCTGGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTT[T/C]TCAACTTTCCAGACTTGGA AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A	G	CTCTGCATTG / GCAAAAAGGA CTGATTAATAA ACTTAA / GCTAAAGTCAG	CATATCATAGCCAGATCTACAACCCCAGAGTAATTCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGT[A/G]ATTAAGTTTATTAATCAGCTGACTTTAGCATTGGGAGATTATTCTGGAT

EST	Pos	A1	A2				Sequence
EST385127	91	T	G	CACTGCACTCT	TGACGATGCC GGGAAGC	AATACTTCG	TAATAAAAACTGACCCAATTGGTAAACTGTGTCTGGACTGAGAGAGAAACAATGAAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCG[T/G]GCTTCCCAGAGTGCAGTGATAACTGTTATAGCC
EST385190	24	C	T	CCTGCACCTCC TAAAAGATCT	TCTGTTAGGAC TTGGGGGA	T	CCTGCACCTCCTAAAAGATCTTT[C/T]TCCCCCAAGTTGCTGCTCGTTTCGTTTTTTGTCCTTGAGAACCTTG AGATGAACGTCATCAATGGATTGTGCTGCTCTCGTTTCGTT TCCTCCCTGATTT
EST385751	66	T	C	GAACATCCCA TGTTTCTGTTT	AGGGAAGGTA GTATAACACAT	AA / CCA	AGTGGTCAAATGTAAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA[T/C]TCTCTTATGTGTTATACTACCTTCCCTTTCTCTTTATACACATAGATTTTCCTTAATTGCAGC
EST386169	101	C	G	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTTGCC		CCATCTAGGCAGGCTACCTGAGCTCTCTGTGTCCCCAGAGTGGGTGCCTCAGCCCCGGGGCCCCGGTGG AGTCTCCGCGGGCCCGGCCCCTGCTC[C/G]GCCACCATCCATTCCTCCAGGGG
EST386528	59	T	C	TCTGAACTGGG CCATTTCAA	TTGCAAAAATG AAAGGAAAAA		TATAGTAGGTACTTTCCTTGCTGCAGCAGGAATTATTCAGTCTGAACTGGGCATTTCAA[T/C]GCGTG GTATTTTTTCCTTTCATTTTGCAAGTAAAAAAATCAT
EST386545	42	T	C	AATGGTCATTT TAATATATCA CGTTTTACA	CAGTGATGGTC CTTAATCTCT ATC		CTCAAGCTGAGAATGGTCATTTAATATATCAGTTTACATA[T/C]AGATAGAAGATTAAGGACCAT CACTGAGGTCACATAGCTCAGAGTTAAGATTTGGACCCAGGCAGGTTGGTTCCAGCATATA
EST387079	75	A	G	...	...		GGATCCTCACTCACCTGGGACAGCCTGAGGAGGGACATCCACCAAGACCTACTGATCTGGAGTCCA CGTTCCCC[A/G]GAGGCCAGCGGGGATGGTGTGCCCCTCCTCCCTCCCAACTCATCTTTCAGGAACACGAGG ATTCTTTGCTTCTGGAAA
EST387592	86	A	G	TGTCTCCCTGA GGGTGATATGG	TCACCATCGTG GACTTAAGG	TAGCAGCACC	TGACCTTGTATTCTTCCACTAGAGGGGGAGAAGAATCACCTACCTTTTGGATGCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG[A/G]CCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAATTCTTGCC TAGCAGCACC
EST387751	40	T	C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	AAACAAACCAACATGGTGG	GACTCTCAACCAAAGAGAAAATCAATAGGAGGAGGATTGGC[T/A]TTGAATTCAGAGCAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCTCCAAATGCCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST388154	91	C	A	TGTTTATGAGA ACCCATTACA CA	GCTGACTGGCA CATGCTTT		CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTTCATTCAACAAG TGTTTATGAGAACCCATTACACA[C/A]AAAGCATGTGCCAGTCAGCAGATTCGTAATAA
EST388584	98	C	T	CACGAGTAAA AAGAAACTCA	GGAGCGGAGTCC AAGGAGAA	ACCGACTGCACTGTTG	TCTTTACTGTGCTTACAACTTCCTCCAAGTTTGCGGTGGTTCCATATTGTTATTGTTATTA TTCAACACGAGTAAAAGAAAACTCATGAC[C/T]TTCTCCTTGGACTCGCCTCCTCCCAATCTCGAT
EST388652	72	T	C	GCTGTGTAGAATT GGAAGGACGG	CTGTGTGTCGATGC AGGACACAG	TTTGTCTTAGTTGTTAA	CCTTAATGGGATTTTACAGCTCATCTGAGTCTCTGCTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGC[T/C]CTGTGTCCTCCGTCCTTCCCCAAATGAGCAGCACATATGCAGGCAGGCAAGAGCAGCATGTGA TTTGTCTTAGTTGTTAA

Marker	Pos			Flank 1	Flank 2	Sequence
EST38878 9	47	T	T C	AAACATCATT ACTAGCCTAG	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAGAACCAAGTAATTAAACATCATTACTAGCCTAGATCCTAA[t/c]TGAGGAGGACATGAGATTT ATTGAAGGGAAATCCTCAATTAATATGAACACATTCTTAATTTATTTGTTTCACTTCTCAAATATCGGATTGTTGC TCATGAGAGGAAATAATGGCTGGCACGGCAGTCTTCTCA[g/c]GCTCCCTGGATAGCTAAAT
EST38882 6b	113	G C		...	...	...
EST38882 6a	35	T	T C	TGTCATCTCAC ACATTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCAATGTCATCTCACACATTCTTTATTTTTA[t/c]TTGTTTGTTTCACTTCTCAAATATCGGATTGT TGCTCATGAGAATAATGGCTGGCACGGCAGTCTTCTCAGGCGCCGTGATAGCTAAAATT TA
EST38909 5	47	A G		GCACAGCATG GCTAAAAACG	GGTATTGTTG ATTCCCATCTT T	GCACTAAACTAACTTTCATTGTGGATTGCACAGCATGGCTAAAACG[a/g]TAAAGATGGGAATCAA CAAATACCATTGAAGATATGGAGCAAAGAGAACTCTCACATACTGCTGGAGGGAATATAATT
EST38911 9	85	A G		GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCCAGTGAAAACACTACACATCAAAACTTAGGGAAATGTGGTTAGTGTGGTACGTTGAG GGAAACTTATAACCTCAC[a/g]GCGCTTGTTTCACAAAACAACAGACAACAGAGATTTCCAACTC CAGCAATGACAGAGGCTAGGG
EST38955 5	30	G C		TGAATTCCCTT GGTTGGG	CACTGCAATCT CACCCCC	TAAACATTCCCATTGAATTCCCTTGGTGGG[g/c]GGGGGGGGTGAGATTGCAGTGCTCAAGATAAA TATCCAAATATCAAAAACTTCAAATTGTCTATGCATTCACACACTGACACTGAGCCACAAACATT CCTTTCACAGGGACTGTAC
EST39002 0	42	G A		GGACCCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGGGACCCTTCGGTGACC[g/a]CAGGCTCCCTGCCAGGGCTTGG CCCCTGACCGGGGCTCGGCGCCCTGACGTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79	T G		GGTGGTAAGG CCTAAGGAATT	ATCTCGGCTGG OGGC	CACGTGGCCCCTAAGTTCCGGGGTCTTCCTCCAGTCTGGATGGCTGTGTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATT[t/g]AGGGGCAGGGGGCGATGCCGCCAGCCGAGATGGTCCTGTAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90	T C		TCCCTATTATT CCATGATATTT TTTCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAAATGTCATCACAACGCAACATCACGATGATATTTCA[t/c]AGCAACTAGTATATATATTTTCACAAACCAT CCCTTATTATTCCATGATATTTGAAAAATATACCCTATTTATTTCTTTATTATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69	T C		CCTTTGTCCTC AATTTTTAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGTGTCTTCATGTATTTTCTCATTCCTATCAGGTTCGGTCCTTTGTCCTCAATTTTAACACT[T/c]CTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACGCTGCCAAATTTCCTCCCAGTT
WI-16406	24	C T		GCTTTAATGGC TACAGAAAGA ATGTGTTTAAA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGAAGAGG[c/t]GGTTTTATTTCTTTTTAAACACATCTGGTTCTCGGCAGC AAGTTATTATATGCATTTAGAGCAATAGGTGCCCTGAA

Clone	Pos	Allele 1	Allele 2	Sequence
EST392360b	57	C	G	TCATCTGAGA ATAAACTTCCT GTCT / CATTATAGGTA CTGAGTCATAC ATTAAACA / TCCTTTTATTCATGATGATTTGTTCATCTGAGAATAAACTTCCTGTCTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATATTACCTGGCAAATGAATGAGGTGTCTC TTT
EST392944	63	G	T	CCTGAAACAG GGATGCC / GCACAATTAA ACATAGTACCG AGAA / CAAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTAATTGTGCTGAGCCAGCAACCCTGAGTTACCCGGCCTTTACCCCACGCC AGCTCTGCTGTCTGCAT
EST393662	72	T	C	--- / --- / AGAAAACATTCTGTCTGATCAGAGGAAGAGATGTATGTAGAAAATCAGAAATCTGACTGAATTCCTAAA ATCTATT[T/C]CACACTGAGAGGAAAATGGAAAAGAAAAATGTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTCAGA
EST393719	86	A	G	CATTTGGATTA GGCGTGAGAGG / TGATTTGAGAC ATTTCACATTT TT / AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAAATTCCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAATGCTTCCTTCTAAAGATTA GACATTGCCCAACCCTGC
WI-17177	23	A	G	--- / --- / ACAAGTGACATATCCAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTCTTTCTTCCTTGTGTTCTTT AGAGCCCTTTTCAGCTCATTTCCTGTGAAGCAAACTGCACGAAGGCCTCCCGTACTCCTCCCCTGGAA G
EST394288	31	C	T	GCTCCCCACA ATTTTGATT / GGTCCCTATG AAGCCACC GGCTGTTGC / AGGTTCCTGGTTGCTCCCCACAATTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGGCCTAGGTAATTCTGTTGCCCTTTGGTCCAGAGCACAATTAAAGAGATCAGGTCT
EST394302	45	A	C	GGCAGAGGAA TAACTGATGTT C / CAGGGGTCGGG GTATTG / AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTTC[A/C]CAATACCCGACCCCTGA CCCAGTACCTTTCCCTGGGGGCTTCCCGGTGACGGCTCCGGTGGAGGATGTCCTGGG
EST394467b	117	C	T	CTACTGACAT AGGGACTTCA GAGTAA / TCCTGGAAAAC TGACATAAACC TTTCCAGGATTGTTCTCCC / AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAATAACAGGAACCTATTTATAT ACGTAAATCACTTTCATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT
EST394652	80	A	G	AATGCAGGAG GGTTGGC / CAATCTCGGCC CCTCT / ATGGTGTCATTAGAGGGGCCACAGGGGGATGGGGGAGTAAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGGGTTGGC[A/G]GAGAGGGGCCGAGATTGGGGTGTTCAGGGCAGGAGGTGGAAGACCAG
EST395010	81	A	G	AAAGATTCCT GTAGACATCT AACATTAG / CACTTGCAATT CTGAAGGCT / TGCTTACAAACCCATAACCATAGGCCATGTGTTCAGACATTCTTGACCAAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAATTGCAAGTGCAAGTTCAAGTCAAACCAATTC
WI-18387b	84	A	C	--- / --- / CACAAAATGGGACTGCTGAAGAGTGGACCTTGGACCTTACTTTGGTGACCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAATGTGCGATG GCTATGTAGAGACATAAAGA

ID	Pos			Seq fragments	Sequence
WI-18387a				CCTTACTTGG	CACAAAAATGGGACTGCTGAAGAGTGGACCTTACTTGGTGACCCCATAC[A/G]TTGTG
EST40601 9	57	A	G	GCTAAAGCATG TGACCCCAT	GTCACACATGCTTTAGCCATACACAGTAACATTGACTGGAGTCTTGTGAAAGTGTAATGTGCGATG GCTATGTAGACATAAAGA
	78	A	G	GCGTGGGAACCT TTCTTGGAAGA AGGGCGTC	TCCCAGGATGGTTTATTCCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGGTGACTCGCGTGGA ACCTGAAACAC[A/G]GACGCCTTTCTTCCAAGAAGGGCGTGGCGATCAGGCCACTCAAGG
EST41935	32	A	G	AGTGTATCAC ATCTTCAGGAT GCACACCCTTC AGGT ACACTGTTA	TCCATTCAGTGTATCACATCTTCAGGATAGGT[A/G]ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTGTTGA
EST43091	28	C	T	CATTCTGGTCT TTATTTTGGA CTA CA	ATGTCATTCTGGTCTTCTTTATTTTGGACA[C/T]GTAGCATGTTTAACAAATCAGTTTTCATAGGCAA CCTTTTGAAACATCAAAAGAAATACAATATATTTTCACAAATTCTCATCACTGTAAATTCA
WI-18420c	108	T	C	TTCCATTAAAC AGGAAGTTTC CC C	AGAGAGACAACAAGAAGAATAAGGGAAGAAATGGGAAGAACAGAGTGAAATTAAAGCAAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTTCCTCAAAAAAAATCAAA[T/C]GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	GAATAAGGGA AAATGGGGAAG TC AA	AGAGAGACAACAAGAAGAATAAGGGAAGAAATGGGAAGAA[C/T]GAGAGTGAAATTAAAGCAAATCTT GGATTCAGATTCCATTAAACAGGAAGTTTCCTCAAAAAAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101	T	C	...	AGCTGATCAGCTGCGTGCTTACTGTGTTTATGTGGCCCAGGGAAGCCAAAGATCAGACACCCTGTC CTAGACAGATTCAATGCACACAACAACAGGAGG[T/C]GGGGGGTCACGGGGGCGGGAGAGCCAAAGAC TAGGGC
WI-18425	81	A	C	CACCCTGTCCT AGACAGATTC CCTCCTGTTGT A	AGCTGATCAGCTGCGTGCTTACTGTGTTTATGTGGCCCAGGGAAGCCAAAGATCAGACACCCTGTC CTAGACAGATTCA[A/C]TGCACACAACAACAGGAGGTGGGGGGTCACGGGGCGGGAGAGCCAAAGAC TAGGGC
WI-18449	129	C	T	CTTTTGGCTCT AAGTGGGACT CTCCCCTGACT GTATCCAGA	AAAATTGAGGTCCGGGTGGAACTATAAAAGGAAGAGAAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTCCCAGTTGCTGCTTCCCTTCTTTGGCTCTTAAGTGGGACTA[C/T]TTC TGGATACAGTCAGGGGAG
WI-18457	120	T	C	CCACAATGGC AGAGGTGA ...	ATCGCTTCATTGAAGCCTGCTGCTTAATTTCTCTCAGTCAACTGTGCCCCCAAGACATTATTTTATTCTT AAATGTCCAATATCTGCCTGATGTCTGTTGTGCACATTGGGCACCACAG[T/C]AAATAGGCTAAA AGGCCAGTCCCACCTGCT
WI-18462	39	A	G	CCACAATGGC AGAGGTGA TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTTGTACACCACAATGGCCAGAGGTGA[A/G]TAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCCTCACAGCAAAGTTTGCTAATCTCGGGTTTAGGCCGACTCCATTGAG
WI-18476	60	C	T	GGTGGGGGTGC GACGATGGGA GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGGTGCCGGAGG[C/T]GGT CACTCCCATCGTCGTGCCCCTGCCCTCCTCACCCACCTGCCCACCACTGGCCCAGTCCCAGCGTTGAGGT

ID	Pos	Allele	Sequence (fragments)	Sequence
WI-18491	109	G A	AACAAATGGT AGGTGGTATT AATACTATT CGTGTGCATT TCTTGTAATCC CGT	CTAATGAGATGAATACATGGAAGGGCGTTTAGCACAGTGCCTAAAACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAATACTATTATTAAATCCCAGAATGAC[G/A]GGATTACAAGAAAAATGCACA CGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT ACCCTTCACCC GCCC	AGCCCCCTCCACTCTGCTTCCACAAAGTCGGCTCCGAGAGCTCGAGGCTGCTTCTTTTTATAT GTGCAGGGCC[C/T]GGGCGGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTTGG ATGGTGACTT GGGGAACCACC CAGG	GATCTTGGAAAGCACTAGAAACTAAACATCTTCACCAGGTGCTGAAGAAAAGTGTCTTCGTTTAAT TGCCAAGCAGGGATGTGGAACATTTGGATGGTGACTT[T/C]CCTGGGGTGGTTCCCCATAGATTCACCAT
WI-16543	67	G T	AGATAAACTA CATTTGGGTTT TGG GATTCATCATT ACAGGGGACTT	GATCCATTACCTAGGGTAAAATTCTCCTGAATGTCAAACAAAGAGATAAACTACATTTGGGTTTTGG[G/T]AAGTCCCCTGTAATGATGAATCAAGAATCCTCAAGTCTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAAGG TTGGGGAA TTACTTTTGTA CCGACCAGCA	ATCTGAGAATGGAAGAGTTCATCCCAAAACCATCTCCCCCTGACCCCCAGTCCATGGAAAAATTGTC TTCCACAAAACCGGTCCTGGTGCCAAAAAGGTTGGGGAA[C/G]GTGCTGGTCGGTACAAAAGTAATT G
WI-17690b	79	A G	---	ACAACATGTGAAAGAAGAGATATGTTGTCTTACTCACAGTGGAGGCATTTTTCTAGCTGTGTGTTTGATTT GGCTTCCCTAT[A/G]GATTCAGGACCCATAACTCTGTTCTCACTCATCTGTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTTC TAGCTGTGTTT CAAGAGTTATG GGTCCTGAATC	ACAACATGTGAAAGAAGAGATATGTTGTCTTCCTATAGATTCAGGACCCATAACTCTGTTCTCACTCATCTGTATGCTGCTG TTTGGCTTCCCTATAGATTCAGGACCCATAACTCTGTTCTCACTCATCTGTATGCTGCTG[G/A]A
EST51717 b	128	C T	GCGGAAGACA GTGTGAGCTGTT TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTATTCTGGGGAGGAGCAGGCGGGAAGCAGTGAGCGTTC[C/T]GAG TGGCAACATCACCCACTACCTGGTTTTCTGGGAGGAGCAGGCCGGGAAGCAGTGAGCGTTC[C/T]GAG CTGGATTATTGCCTCAAA
EST51717 a	39	C T	---	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTATTCTGGGGAGGAGCAGGCGGGAAGCAGTGAGCGTTGAG CAATGGCAACATCACCCACTACCTGGTTTTCTGGGGAGGAGCAGGCCGGGAAGCAGTGAGCGTTGAG CTGGATTATTGCCTCAAA
EST53012	97	C T	TGGTCACTTTG GGGCC GGCTCTGCCCA CGCC	TTTCCAGGTTGACAGGTTTATTCCACCCCCTTCCATCCCCATGGCCACCCCCAGGCAGGAGGAGGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGGCC[C/T]GGGCGTGGGCAGAGCCCACTGGGTTTACATTCTCTGT GGGGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC CATCTGGATAT CTTGTCACATT TT	AAACTGCAAATAACAAAACAAAACAGAAGTCCAAGAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAAA CA GCCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGACTTGACAGCTGAGACGCAGCAGGAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAATAGGTTTTAACATGAAC ACATTAAAGGGGGATGGCC

EST	Pos	A1	A2		5′ flank	Sequence
EST53477	61	T	C	...		TTTGAGAGGTTGTGCAAAACTACTGTATTTACAAAAATGGCACAAAAGTGAATTCAACAGT[T/C]AATGCACATGCATACTTCATTCACATCTTCAACAACAAAAGGTATTCTAACTCTACAGAACTGAATATTAGCTTCAACGGCAGCTGTT
EST64622	91	T	C	CGAGATTTCT TCTTTATTTTA TATTTTTCA	CCAAAGAAAA TGGCTTCAGTA A	GGGGAGAGGAGGTAGATTGCCAAATTGCCATTTTTTAAACTCCCGAGATTTCTTCTTTATTTTATATTTTCATTTTCATCCTAA[T/C]TACTGAAGCCATTTCTTGGTTAACTTTAGA
EST67268 a	77	C	T	TGTGTATAGCA CATACTTCAGG C	ATGGGGTGGTG CCGC	CTCATCTTTATTAAATGCATCGTGTGTGTGTCTTCAGGC[C/T]TGCGGCACCCCATAGAGATGGTGAGGAAGTAACTTCTGCTTCATTGAAACT
EST78503 a	26	C	T	ACGACGCCGG CGAGT	GCATTTCCGCG GCAC	GAAATGCAGAACGACGCCGGCGAGTT[C/T]GTGGACCTGTACGTGCCGCGGAAATGCTCCGTTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGATGAA
EST80253	92	G	C	...		ATGCACTTTATTGGCTCCCAGGGAGTGGGATGCAGGATCAGAGTGGACACGCGCAGGGGGCTGGTGTGGGGGACAAGCGGCCGGGGCCTGCCCG[G/C]GACCCTGGTTCCCTGAGGACCAACGTGAATGGGGGCCCCACTGGAAAGATGCTTG
EST91254	73	T	G	...		TATTCTGTAGGGAGAATAACCATGCTTGCTTATGGACTATCCATGGATAACTTGGTTTTTTTGTTGTTGTTGTT[T/G]TTTAATTATAAGAATAATAATATGTGCTCATCATATATGCCTTTCTCAGTAGAGCCCAGACCTGG
EST91332	100	T	A	...		TCCAAACTGAAAGGAGGGTGGGGAAAACAAACGCATCATCATATGTAAAGCACTGAGTCCAGCCTGGCTCTTAGTAAGCATTTTAATCACCTTCAAAAATTAA[T/A]TGTGACTTACGGAAACAGGTCACTGAATATTATT
EST91495	58	T	C	...		CTGACTCAAAAGACACTCCTGAAAGCAGGTCCATCCTGAGCAGCAGCAGCTTGTATTACTT[T/C]ACAAGTCAGAACCTGTTATTAAAGACGGACTGGCATTTAAATCAGGCTGTGTCACCCCATCCTGGGTCTTTGTTCTCGGCTCCTATGGTG
EST91921 b	114	A	G	...		CTGGCTGAGGGATCTCAAAAGACATTCCACCACATTGAATCTTAGGCTGGAGGACATTTTCGTATTCTTCAGTCAGGAATAGCACACTTCCTTCATGAATGAGCAGCTTTTAGGG[A/G]TTATATCATGAGGTACAAATAAAGAGGCCCTCACC
EST92026 a	56	T	C	...		ATAGCCAAGATTTGGAAGCAACCCGTGACCATCAACAGATGACTGGATAAATAAAA[T/C]GTGGTACATGTACACTATGGGAGTACTATTCAGCCATGATGGGGGAAAAAGTCTTCGTGTTCATTAGCAACAACATGGATGGAACTTGGGAACACTGT
EST92040 b	38	C	T	...		TTTCCATGAGGAATAAATTTGTGTTGTTATATAAAACCTG[C/T]AGATGAATATTTTTTAACAGCATGATTCACAAATGCCAAAAACAATGCAAATGCCCTTCAACACATGAATGGATTAACAGACCGTGATACATGA
EST98276 c	69	T	C	...		GAGTCTTGCTATGTTCCCAGGATGGTCTTGAGCTCTGGTTCAAACAATCCTCCTTCCTAAGCCTCC[T/C]AAAGTGCCAGGATTATAGGTGTGAGTCACA

EST98276 b	61	A	C	...	...	GAGTCTTGCTATGTTTCCCAGGATGGTCCTGGAGCTCCTGGGTTCAAACAATCCTCCTTCCT[A/C]AGCCTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98276 a	22	A	C	GTCTTGCTATG TTTCCCAGG	AACCAGGAGCT CAAGACCA	GAGTCTTGCTATGTTTCCCAGG[A/C]TGGTCTTGAGCTCCTGGTTCAAACAATCCTCCTTCCTAAGCCTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98800	53	A	T	...	...	GCCTCCAGCTGCATGACTCCTAAGCCATCATTCGAAGATTTGGCTAATTG[A/T]TAGTCTTACAAAGGCAGTCTAGTTCACCAGGCAAGAAGGGGGTTGTGTTGGGAAAGCGCTGCTATCTTTGTTCAAACTGTAAAGCAAGTTCCTC
J02931	138	G	A	CAGCATTAGTC ACTTTGAAAT GTAA T	TTGGAATTGGT TGTAGTAGTACCAT T	AGAGGATAGAATACATGGAAACGCAAATGAGTATTTCGGAGCATGAAGACCCTGGAGTTCAAAAAACTCTTGATATGACCTGTTATTACCATTAGCATTCTGGTTTGACATCAGCATTAGTCACTTTGCACATTAAC[G/A]AATGGTACTACAACCAATTCCAAGTTTTAATTTAACACCATGGCACCTTTGCACATAACATGCTTTAG
L41680	88	G	A	GAGAAATCGA CTACCAGCTG A	TTTAGAGCACT TTGCAGGTATT T	GGATCCAAAACACGGCTGGGTTCAGCATCCACCAATGAACTGAAAGGTGAATAAAGGACGTTCATGAGAAATCGACTACCAGCTGAT[G/A]AAATACCTGCAAAGTGCTCTAAAAATTAAAATATTTTGACTTTAAGGGTCCTAGTAAGTGCCACTTCCACTAAGAATACAGTTTGAATGTATAATCAGTAGTGTTTACAAGATCCAACAGTGCACTCA
M15796a	84	C	G	CAAATTTGTA CCTCTAAGTAC ATATGTAGA	TTGGACTTTAT TCTTTAAACAA ATTG	CTTTTCTGTCACCAAATTGTACCTCTAAGTACATATGTAGATATTGTTTCTGTAAATAACCTATTTTTTCTCTATTCTCT[C/G]CAATTTGTTTAAAGAATAAAAGTCCAAAGTCTGATCGGTCTAGTTAACCTAGAAGTATTTGTGTCTCTTAGAAATACTTGTGATTTTATAATACAAAAGGGTCTTGACTCTAAATGCAGTTT
M20472	103	C	T	GTTGAGTTCTT TGGGACCAAA C	ACAATGAACA ACTCTAAAGAC AAAAA	AGAGCCACCCTGTGGAAACACTACATCTGCAATATCTTAATCCTACTCAGTGAAGCTCTTCACAGTCATTGGGATTAATTATGTTGAGTTCTTTGGGACCAAAC[C/T]TTTTTGTCTTTAGAGTTGTTCATTGTTGTGATTGCATGTTCCTTCCCTTCCTCAACTGTGTTCTCCCTGGCCATTCAGAGGAGGAGGAGGAGGAAGA
M32315b	129	T	C	GCCTCTGCTGC CATGG	GCCTTCCGAGA GGGACAC G	CCCTCTGACCTGCGCAGGCCAAGAGCGAGAGGCAGAGCGAGTTGGGGAAAGCCTCTGCCATGGT[C/G]GTGTCCCTCTCGGAAGGCTGGCGGCCATGCGTTCGGGGCGCATGCCCTGACTCTCTGT G
M33875a	131	C	T	GGTTACAGCTG GAGGTGTGT	ACCTTTGTTAA AATTTAGGTGG TTAT	TTCCCAGGAGGAGCAGCAAAGGGGCCTGCTGAGCCTCTGGTTAGGTTACAGCTGGAGGTGTGTATATATATACACACACACGTGTATATACACATATATATGTGTATGTGTATATATATATGTGCTTTT[C/T]CAATAACCACCTAAATTTTAACAAAGGTTCCTTCTAAGTGGTAGAACTTGGGGTGGTATTTTACCTTCTTCT
TIGR- A003M18 a	29	A	G	TTTTTTGTAGAG ATGAGGTTTTC GCT	GGCAGACGGAT CACTTGA	TGTCTTTTTTGTAGAGATGAGGTTTTC[A/G]TGTTGGCCAGGATGGTCTCGAACTCCTGACTTCAAGTGATCCGTCGCCCTTGGCCTCCCAAAAGTGCTGGGATTATAG

Clone	Pos			Sequence
TIGR-A003P30	117	C	G	ACAAGTTCAAAAGGAGAACTTCCTTGTTTAATGCAGCTGTGCTCAGAAGAGCCTGTGATTCCTAGGAAACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAAGGTACCCTTGGAGATACT
TIGR-A004S34	156	C	T	GCTTGTCTTTATGTTTAGGTTCGGCGGGGAAGGAGAAGGGGCTGCAACCGCAGACATCTGGACACCAGCAAGGGTCCAGGGGGAGGTTTGCAGAACTTCTTTGTCCTTGGCTAACAGTCTGTCATGGACAATAGCCAAACCTCCTATAAA[C/T]CTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTTTACATG
TIGR-A004T44b	97	A	C	AACAACAGTGTAATCTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGATTGAGTATGATAAAGAATTTGCATGGCGATT[A/C]AATAGAAAACCTATAAAGTGTAGAAAAAGCAGGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR-A004T44a	69	G	A	AACAACAGTGTAATCTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGATTGA[G/A]TATGATAAAGAATTTGCATGGCGATTAAAATAGAAAACCTATAAAGTGTAGAAAAACAATATAGGGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR-A004V08	60	T	C	CCTACAATCCTATATATTGCAAGGGTGGGAAGGATGCAGGAAAACAGGCATTCTCTTA[T/C]GCCTTTTGTGGGAAGGATCAATTGGGGCATGCACTTAGGGCAGTAGTGTCAAATTTCAGTAGCTGTCAAATTTCAAA
TIGR-A004V26	125	A	G	TCTAGCTATAAGACCAGATTTAATATTCTAGATATAGAATTATCCAGAATAATTCTATTGAATTGACTGATTACAAAATGTTAACAGCTGGATAAACGGTAAAATATGCATTATCTTCACATGA[A/G]AAGGTTTCAGTTTATAAATGCTAAATACTGTATATTGCTTAAAATACTGTATCTATGG
TIGR-A004V28a	29	A	G	CCAGGCTATAATGTTGTGGGTGCGATCTC[A/G]GCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCTTGAGTGCCGGGACTACAGGCACCCGCCACCTAACTAATTTTTGTATTTTTAGTAGGACACATTGTATTTTTAGTAGAGACAGG
TIGR-A004X20	25	T	C	TAAGTTTTCCTTCCTTCTGTGTAGGA[T/C]GTCTCCATGTTACAGTCAACTATAAAACATGGCTCATGTTCACTCTGGGCTTCGGCTTCAGAGGAGTTGATATTTGGAAGTTGTACCTTTGTTCGTGTGTGCTTTTCAGACCAACCGCCTTCTTCTTCCAAAGGAGTTAAATCATCATCCATGTCCAATCATCATGTCCTT
TIGR-A004X30	26	T	C	TTTGAAATCTTAGAGTAGAGAACCCACT[T/C]ACTCTAGTAATACTTGTAATAAAATTAAAAATAGTTTTAGAGTTAAAAAACACTTCCATAAAGAATTAGGGGGTGCCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCATGTTAGGGGATAAAGATATCCATGTAC
TIGR-A004Z04	102	T	G	CACGGGTATATGCCTTATATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATGGGGTCCACAGTACCTTCTTTCCATATTCAATGACAATTATCAAAAAATACAGTCTCTTTAGTGATTTAAGAGTC

(Note: additional short fragment columns associated with entries: TIGR-A004S34 — CCAAACCTCCT / CATTCCTATAAA / A; TIGR-A004T44b — GGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG; TIGR-A004T44a — GGAAGATAAA / CCAAAATGAT / TGA / TTCTTTATCA; TIGR-A004V08 — CAGGAAAACA / GGCCATTCTCTT / TCCTTCCCACA / AAAGGC; TIGR-A004V28a — TGTTGTGGGTG / CGGAGGTTGCA / CGGATCTC / GTGAGC; TIGR-A004X20 — AAGTTTTCCTT / CTCTTCTGTGTAG / TTTTATAGTTG / ACTGTAACATG / GA / GAGAC; TIGR-A004X30 — TTTGAAATCTT / AGAGTAGAAC / TTCTTTATGGA / AGTGTTTAAAA / CCCAC / CTATTTT; TIGR-A004Z04 — CTTATAATTAG / TTCATTTGGGT / AAATTTCATGA / ATGCAAAACT / AAGCAA)

ID	No.			Frag. 1	Frag. 2	Sequence
TIGR-A004Z19	85	C	T	GAGAACAACT TTTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAGAACAACTGC AGCATTTTTCTTTT[C/T]TCTTCCCGATGACCATCTTTGGGCTGGCGGGCCAGGCCCTGGGTGTC TCCCATATCGCTGTCTTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR-A004Z42c	89	C	T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCCG GTCC	GTCTTAGCAGGAGAGATAACTTTGAGGACAGCAGCCCCAAGGCGCCAGGTAGCCTTCAGGGGCGGGGCA GGGTTGGGGGAGGTAGGAGACT[C/T]GGACCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCCTT CATCATCTGTGTCTTC
TIGR-A005D17c	81	T	C	---	---	TATGGACTGTGTAGAAATATGATTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC[T/C]GTCTAGATTCTTCTTGGCCTCTCGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACAC
TIGR-A005D17b	79	G	C	GGGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGGG AAACCCAGCAAG[G/C]GTCTAGATTCTTCTTGGCCTCTCGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACAC
TIGR-A005D44	97	G	T	TTAACATTATT GAACTTAAAA CTGTTACAC	TTGTCTATTAT TTAAAGCCAAC AAAA	CATCAGTAACATATACACAATTGGTCATCAACTGAACTTTGCCTCCAATATATTCTATACAATACTT AACATTATTGAACTTAAAACTGTTACACT[G/T]TTTTGTTGGCTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAC
TIGR-A005E31b	27	G	A	---	---	GGAGTTCAAATTTATAACCAGGCCTCT[G/A]CTCACAGCTGTACTGGCTAGGCAAAGCTTTCCAGAC ACAAAGCCACCTGCCATGTGGATAGTACTCTTTGCCTGCTTGCCCCTACAAAGCCACCTTCTAT TTCATACCAATAACCTTCTATTCATACCAATAAG
TIGR-A005E39	182	G	C	AGTAAGGTTA CTGCACCTTAC AGAG	---	CTCAGTGTAAAAACTTTGTTTAGGGAGAAAAAAAAATCCAATGGATATATGGGAAGAGAGAAGTG CCAGGCTGGATGGTGCTGAGACAGAATGACCCCTTGGCGTCCTTATTTGTTCTTTCAACAGGACC CCCACAGATATTTGCGGTATGTCATGGGGACTGGGGATGTCTTCTATTG[G/C]GGATGTCTTCTATTTT
TIGR-A005E42a	42	A	G	CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAG[A/G]CTCAATTCCCCTGATTTAGGA AGGCGGATGCTAAGGGTATTGCATAAGTGTAAAAATGTTGTATTTAAGAGAATCCCACAAG CTTGGTATAAGGCAGAAAAATAAATAGGTATAAGGCAGAAAATAAATAG
TIGR-A005E46	76	A	G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATGATATTAGCTACCTCACAGCCAGGGTTGGCAAATGGTCATTTGACAAATGGTCATTTG TGCTTTAC[A/G]TACATTACCTCACAGCCAGGGTTGGCAAATGGTCATTTGACAAATGGTCATTTG ACAC
U20979	24	C	T	A	GCAGGGGTGA CGTATGTGAGA CCTAAGC	GGGGAGGACAC CCTAAGC	AGAGCAGGGGGTGACGTATGTGAGAA[C/T]GCTTAGGGTGTCCTCCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCCTGCTTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGTAAAAATTCCCCAAGAGCCGCCATATGAATCTGTCCCC

ID	Pos	A1	A2	Sequence
X57830	106	G	C	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTCACCTATCTGTGAAAAAAATATGAGATTGGAAAAAATTAGACAAGTCTAGTGGAACCAACGATCATATCT[G/C]TATGCCTCCTCATTTTATTCTGTCAATGAAAAGCGGGGTTCAATGCTACAAAAATGTGTGCTTGACAGCATTTCAGCTGTGAGCTTTC
X74070b	72	T	G	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAGAAAATTTTGTTTATGGATCT[T/G]GATAAAATCTAGATCTCTAATATTTTAAGCCCAAGCCCCTTGGACACTGCAGCTCTTTCAGTTTTGCTTATACACAATTCATTCTTTGCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTTGAA
Z48804	44	C	T	ACTGCCGAAGTGTAGGCGGCCCCAAACCTTGCTCTCATCACCAGC[C/T]TAGAGCTTCTTCCCGAAGGGCCTTTAGGATAGGAGAAAAGGGTTCATGCACACACGTGTGAGAATGGAAGAGCCCCCTCCAGACCACTCTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCGTGTAAAGTAAGTGTAAGGTCCA
D28513b	133	A	G	ATGACCAAAGCCACCACATTTAGAACTTTGGCGTGCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCCCGCCCCCAGAGGGTCAGCACTTGGACATGGCTCACAAGCAGTTTTGATTGACTGCATGAATGC[A/G]TGTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGAGGCTTACATATAATTTAACCAGTTCTGTCTTCAGCTGTACATA
D29833b	85	A	G	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGGACCTCCATTTTCCCTGTAA[A/G]TTCTCCAACTGATCCTCCACCTCCTGCACCCCAAATATGAACAACTGCAGCAGGTGCCACCACCAGACACCACCCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A	G	CCACTCCATCCTGATGCCCCA[A/G]GTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGGACCTCCATTTTCCCTGTAAATTCTCCAACTGATCCTCCACCTCCTGCACCCCAAATATGAACAACTGCAGCAGGTGCCACCACCAGACACCACCCTTGTAACTACTGCTTCTGCTAC
D31762	82	G	A	CTCCCTGCCTCCTCCTCTGCTGTGATGCTCCGTCCGGAAACCTGTCTCAAACAGCCGAAACCTGTGTCTTGCAATGGGGGGAGGGGGGCGTTTC[G/A]CTTTCCTTCTTCTTGGCTCCTCTATTCTTCCACAAACCATTCTCAATAAAGCCAAAAATCTTTCTCTTCTCCCCCTCCTGTCCTGTCCTGTGCCTGGCTTTTCTGGA
D37931	64	T	C	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAAATAGCAGTGAGTAATGCATTTGAGCTGT[T/C]CCCAGGCTCTGTCTCCTCAGCTCATTCTCCTACTCTTTTCTCTATAAATACATTGCACCAAAGAGAGATATGGAGACATAAACCTGTAATGAATGAGGCTGGCTTTTCTGTTAATAAGCTTCCTTT

ID	Pos			Sequence
D63807	101	C	T	CAGGCAGGACTTCAGTGTCAGTATCCCTGCCTTCAGTCTTCTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGGTGTATTTTCCTGTTCCA[C/T]GAAGAGGACTTTTGTTCACAATTGGATCAC AATGCAGAGGAGTCTGTTCCTCCCCGTCGGCTTCTCGGTGCTGTGGGGAGGTGACCTGTCCCAGATGAC
D90145	21	T	C	TGGGAACATGCGTGTGACCTC[T/C]ACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGTGGGACTCTCTTAACTTAAATTTATTTATTACTATTTAGTTTTATAATTTATTTTGAT TTCACAGTGTGTTTGTGATTGTTGCTCTGGAGAGTTCCCCTGTCCCCTGTCCCCTCCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	T	C	ATTATCACTCTCAAAAATTTGGTGTGTGTTAAGTACTTCTTATTTATGAGCCCC[T/C]GAGGA CCAGACATGTATTATCAAGCACCCTTATATACCATCTAAT
EST16668 5	71	C	T	GCATTTAAAATTCACATTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATT ATG[C/T]TGTAGATTTCAGATGTAGGTCGTCAATACTGAGCACTTATCT
EST16904 7	57	C	T	ACAGACTATCGCCAACTTATAAATGCTTAAACTTTATGATCAATAGTAATAAATTACA[C/T]GAGATA TTCACACTTTATTTATAAAATAGGGTTTGTGTAAGATGATTTTTCCCAACTGTGTAGGTTAACAT
EST21863 9	49	A	G	TTTTAAGTACCAGAGGCACTGCTGGAACAGGAGTGAAAACTGATACACC[A/G]GTTACTTACTC TTCACTCTTCAAACTGATTCCCCTAAAGAGACTTCTACTTAGCAAA
EST21885 6	80	G	A	GGCTGTAAGTAGAATCAAAGGTTAAGAACACATTTATGCACTTATTCCACAAACATTTACTGAGCATA CTAGGTGCTGGGA[G/A]TGTGACAGTGAGCAAAAAACACA
EST22623 8a	26	A	G	ATTTTAGTGCAAATGACAAAGCCCAA[A/G]AGAACAGAGGATCAAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTAACACAAGTATGGGAGT
EST22644 2	98	A	G	AAAAATGATTGAATTCAGCAAGTACATTTTGATCTATCTACATTGTTAAAACAGCACTAAAAATAA AAATTTTTAAAATGATTATCCATTATTTACAG[A/G]AAATGTGGAAAAGATGGCTTTAAACCC
EST23587 1	31	T	A	CCTCATTTATTTAAAAAGACGGACATAAAAAA[T/A]TATACAACAAAAAACCCAAGTCACATTTCAG GAGGTAAAAACTAAAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106	T	C	AAAGATCTGGCATTATTCACATCATCCTCTAAATATTTGTAATTACTTTTTCCATGAGTATTTTTTCA TGTCCAAGCATTTAACTATCATTTAGCGTAAATACC[T/C]GAATAACCCATAGTTACAGAATTGG GTCTGTGTAACCTCAATT
EST24308 3	45	A	G	TAGTTTAATTTCTGAACCTTGGCTTATAAATTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAAATATAAACCTCGTTC
EST24435 6	73	G	A	CTTGAACTTCTGGTCTCTCAAGTGGTACGTCCGTCTCCAAACCTCCCAAAATGATCGGATTACAGGCATAAG CAGCCC[G/A]TGCCTGACCCACATTTCTTTATCCGATCTGTTGATGGACATTCAGGTTGTTTC
EST25089 6	25	T	C	TATTGTTGCATTATCAAAATGGTTA[T/C]AGTTTTCAATTAAAACTGTAATTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAAATGTAGTTTCCAATCGTTAGTTAATGCTCACATT

EST	Pos			Sequence
EST254769	33	G	A	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTCCTCCTAAAAAACCAAACACAGAGGTCCTCTGCTCCTTTCCATGGCAGCCCTCTGCTCCGGCGTGTGGACCGTCTGCTGA
EST261832	70	T	A	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTGATTAACTTGTAAAGATTGATCTCTAAATAAGATT[T/A]ACATTCTGGGGTACTGGGAGTTAGAACAAC
EST272311a	28	T	C	AGAAAATAAGGTGCTACCAGAACTCATGT[T/C]GATAGCGCTTTCTTCTTTTAGGCACATATTATAGCATTCAGATGAAAGTTCTGTAATCACACACACTGTGCCTCTAACAAACACGGTGACTCTGA
EST278165a	26	T	C	CAACTCAAGGTACAAGAGACAATTGCAT[T/C]TAACATTGTTATAATAAAAGGAACATCAGATCAATCATTAAGGGCTCCAGATGAACAGCATCTTCATAACTTCCATGTT
EST285880	78	A	T	GTTTAATTGGCGTATGGTTCCACAGGCGTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAAACTTACAAATCA[A/T]GGTAGAAGGCAAAAGAGAGAGGAGAAGAGAGGCATCTCTTCCATGACCACAGCAGGAGGAACAGACAGAGGAGGGGGAT
EST302265	25	A	C	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAACTTCATTGTAGTAGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAGACAGACTCATTTCCTTTGAG
EST309359a	59	C	G	AGCTATGGTAGAGCAAATTCCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGA[C/G]AGGTGTTTGAATGTCAAGGAAATCACTGAGGTAGTAGTTGGGATTACAATAAGAGACAGCTGCCCTGTGAGGTCATAAGAGCTTTGTGAGG
EST325157	25	G	A	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCTCTAAAACCTGTTGAATAGAATAATGGCCAAATATTACAGTTTCTCACTTCCTATGAATACTGGCACTGTTTATTCATGTTTATATGTGAGTTTCTATGCATAAAAATCCCAGTAAGA
EST332744	27	T	C	TGCTTTGTTTCCCTCCAAATCCTAAAA[T/C]GTGTGTCTTCAAAGAAATTCGTGGAAAGGACTTTGAATACGAGTTTGTGTACCATTGTCCAGTATTCTGAATACAGGTTTCAGATAACTATGGAGATAACTATGGAGAGATATACCATTGGACTAGGTA
EST333527b	75	C	G	TACACATTATTCAAGAGACCCACCTGACATGCATCTCCTCCGCAGAATACATTCGTCTCCTCTCTTAGAGAAGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGAATATCTTCTTGGTGTCATATCTAGGGG
EST334241	126	A	C	ATTTTCCCACAGCAGAAGTAGAAGTATATTATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGGGAACCAGTAGTACAGAGATGTTCACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAACAAGGTGTTGAATCCTCTT
EST334887	90	A	G	CCTTTGGGGGAGTTTAAGCCAGAAATGTGACAAAGTCACTTACAGGAAGGAAGACTGGAATGTAGCCATAGTTGAACTCTAACATCGTCTATAGA[A/G]ACCATTCCCGTCGTCCAGTTGATACTAAGCTGCTC
EST335081b	45	C	T	AAAAACATGCTATTTGAACAAAACTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTAAATAACATCAACTCACAAATGACTTTAGAAGCCAAATAA

EST	Pos			Sequence
EST33508 1a	36	A	G	AAAAACATGCTATTTGAACAAACTTTTTATAAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTAAATAACATCAACTCACAAATGACTTTAGAAGCCAAATAA
EST33863 4	77	C	T	ACAACATAGGACTGGTTATTCTTGGTTTGAAAAATTATGTTGCCACTTCCTATTGTTTTAAAAATGATCATTTAAC[C/T]TCTTTGAACTACAGCCTGAATCCCCC
EST34739 3	97	T	A	GAAGTATCCTTCCCAGTGGCAGGAACTGAAGACTCCAGATCAACCAGGTGGACCTTTCGTTGATGAGCTGATAGCTTCTAGGCTGTGTGGGGAACCTC[T/A]GGTGCCTTACAACTCCAACTACTGCAGAATTTCTTGTTGTGCCTCATAAACA
EST34792 6b	104	A	G	ACCTGACTGCTTTAAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATACTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCTTAGTCCTATTACAAAGATTTTGTTGCTGTG
EST34835 9b	93	T	G	GGAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTGTGGGGAGTCTATGTGTTCTGG[T/G]GGGCCTTAAAAGAAACAGACAAATTTGTCTAAAGAT
EST34835 9a	82	G	A	GGAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTGTGGGGAGTCTATGTT[G/A]TGCTTTCTGGTGGCCTTAAAAGAAACAGACAAATTTGTCTAAAGAT
EST35230 0	93	G	T	CACAAAGGTCCACTTACTTACATGAAGGAACATAAAGGCATGAGAAAACAGTCATCTCAATAAATGCAAGACACATGAGAGCATAAAAGAGGTTCTC[G/T]GCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33	C	T	TCTTTTCAAATTTTTGATGTAGGCATTAATG[C/T]TATAAATTTCCTGCTTAGGAATGTATCTGCTATATCTCAGAAGTTGGGCATGTTGTGTTCCATTTTACTTAGTTCAGAACTTTTCAATTTCATCT
EST35708 9	32	C	T	CTGCCCCAAATTAACTTTTAGGCAAATGGAAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAGACAGCTTAGTATATGTTCATATGCAGCGTGTTGCTCCCTCTGAGGTTGGCACCTTCCTGTGTGATGTGCAAAGTGTGGCT
EST35747 9	51	C	G	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAACGTTTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCGCCCCTTCCAGTAGGGTTGAGATTG
EST35751 9	89	C	A	TGGTCCATTATATTAAAACTGAGGGAACAAACGGTGCTGACATGGCAGACATTTATTTCAATGGAGAAGTTCCTCCCATGAAACCAAGA[C/A]CTTGTCCTCCTCATGAGATAAAGTGGAGACAATAAAGAAAGCCAGGTATATAATTAAGGCCCTGTGA
EST36301 4	93	C	T	CACCTGTTGTTCATTGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCTCAGCCTACAGCAGTCAGGAGGCAGCCATGCGCCCCTG[C/T]GCTGATGGAGCTTGTTAATTTAGCCCCAAACTGATCTTCAGAAAGAGGTACAACAAA
EST36519 0a	33	G	T	GCCATCAGCCCACCAAAGACATGACTACCAACGC[G/T]GGCCCCTTGCACCCATACTGGCCTCAGCACCTAAGACTGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTCTCTGTCACAGGGGTCTTAGTCGT

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EST366206	50	G	A	GACTTTATTAGATAAGGGGTTTCGGCTACCCTCAAAGTCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAAAAATACAAAAGGGCCACACCGATGCAAAGACTTT
EST366900a	89	C	G	CCTGTGATGTGCATGGGGTGCCTGAGCAGTGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGGATTCCTA[C/G]AGGGGACATATCAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST367299	62	C	T	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACTTTAGCTACCCTGGACAATGCTATCAAGTGTCTGGGAAGGGAG
EST368236	103	A	T	ACTGTCTGGCCGATGATTGGGAGCTTGAAAAAACTACCATGCCAGAATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTATGTTCCTAAGCTCATCATGAG TTAA
EST369874	126	C	G	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST370543	88	T	C	GGTCTCACTCTCTTGCCCAGGACGGTTGAAACTCCTGAGCTCAAGTGACCCTCCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACCACCTGGTTCCTGGTTTAAAGTAACCACTGAA C
EST372693b	105	T	G	AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTGGGATTTAAATTAAGATTGTGAACATG CAAACCCAGCAAATTTCTCAGCTTATATTTTGAAAGTCT[T/G]CAGGAGAAAAAATGGGGTCC
EST372842	93	G	T	AAAAGACCCTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAAACCCTGAGAATGAACCCCT CTTGGCTTGCTTGAGGAATA
EST373152a	90	A	G	AGATGGGGTCTTGCTAGCTTGCTCGGGGCTGAACTAAAGATATCCTCCTGCCCTCAGCCTCCCAGGTAGT TGGAACTATAGTAGGAGTATCT[A/G]CCCTGCCCCTGCTAGAACTTCAAGTTTTGATGGGGCAAATCCA CCCCAGAGGACAGGACAA
EST373741	45	C	T	CCTGCCATGATAATGTTAAAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTAGTTGAAATATTCCTTCACATAGCCAACACATTTTTCAAGGCACTCTAGCTACTACACA GGA
EST373768b	101	G	C	GTGACATCATGTCTCTTCAATTAATAGTAGTTGAGCGCTGGGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGCTGTGTCCTGCA[G/C]GCTGCTCCTCCAGGCAAGTTGCTGACTTCTCTG TGTCCAGG
EST373768a	41	T	C	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGT[T/C]GAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGTCCTGCAGGGCTGCTCCTCCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST				Sequence
EST37378 9	63	T	G	ACACACAAAAAAAATGGTGGCAGAAATCTGGAAAGATTCTAATAACCTCAATTCGTGAAAAC[T/G]AACATGCCTCAAAAAAGAGGGGGAAAAACTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46	G	A	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTAAATCAACCCTTAAATCAATGACGTAGAA
EST37613 6	34	A	G	CTAGGCATGGGGCTTTACAGTCATTTATTTACC[A/G]GTCATGAATTCATTAAAAACCACAGCGAT ATAGCAATGAGCAAAACAGACCCTCCCCAAAATCACCCTGCGTTCATGGATCTTCCATTCTAA
EST38025 4	56	T	G	TTATTGAGTAGTACACTGTGGCCAGAACTAAGCTTTACATGTTTATATCACTTA[T/G]TTATCTCA ACAATCTTGAAAGGGTGGTATTATTTCCCCGTCTTATAGGTGAAGACTCTGAGGTTCAGAA
EST38068 6	57	C	T	TCTACCAGGTCACCAAAGTATCTGTATATGCTTAAGTGGCATTTCATGTCACTTA[C/T]CGCATGG AAGAACGCTCTCCTTTAATTCCCTAACTCTCTTCTTCTGGGAAGAACAGAACGTGCACAA
EST38420 6a	100	T	C	TAAATCAAGGCCTCTTCATTACCAAAACAAAACAAAACAAAAAAAGGAACAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCATCCTGACT[T/C]GTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCCTCTCTCA
EST38950 5	25	T	C	TTTATTTGCAAAGTAAGCAGCCGG[T/C]CTGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAAATACTTGGGACTTACATTTGACACAGGCTAAAAAGTATGGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90	T	C	TTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGGTTTAATATATCATTTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATGT[T/C]AAACAAGTTACTGAATATTTTCACCTCGTGGAGTTG
EST39331 1	70	G	C	TCCTTCTTGCTCTCTAGCACTCAGACCACCAAAGAAGAGCCTGGAAGACCATGGAAGGAAAGTA TGC[G/C]GTGTTTTAGGGAGAGCTGGCACCTGGCCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C	A	GTCACCATTGACCTTACATAGTGCCCTCTAGT[C/A]ACCTATGAGGCACTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTGAAATTT
EST40548 4	37	T	C	TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTC[T/C]TCAAAATAACTGAAACTAAATCTGTA AGATAAAAATGCTGGAATTTGAGAAGGCACACTGCCCTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTTC AATAATCTGTGGGACTCA
EST40549 1	42	A	G	TGTTTCTCTAGAGAACCCTGTGTGATGATCACTAGGCATGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTGTTACCACCATTTCTCACTTGAACCTAGCTCCCTGCAAAGCACCTTCTA CCCTGCACTTTGGGGAG
EST40579 1	81	A	C	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTCATTCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAAA[A/C]GGACTTGGAGACAGCGATTTAAATACGAACAAGGTCTTCCAGGAAG
EST40584 3	68	A	G	TTGTATGGTTGTGAGGAATTTGGGAAGAAGAAATTATCTGTGAAGAAAATTTGCCACTGTAATGCACACCC A[A/G]TTCTGTACTCCCACAATATCCTATGTTTAAGCT

EST51340	51	G A	GATCAAACTGTATTGCCCAGGCCAGCTCCTGAAGAACTATGAACTATGAACTGTGAACTATGAAC[G/A]TCTCAGCCTAGA AGGATAAATGTGACCTTCAATTGCACACCATCCATTGTCTCTTCAAACTAAGAGCCTCTCAAGCTA GATAGGCCAAGGATTATT	---
J04162	134	T C	CATGGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCGCCTCTCACAAGCAGGAAAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA[T/C]TTTTCCTTGGTCTCCAGTGGAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCAGTGAGT AGCTG	---
K01506	63	T C	CTGAAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTTCCACTTCATGTGAAAACTAC[t/c]C CAGTGGCTGACTGAATTGCTGACCCTTCAAGCTCTGTCCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTCCAACAACAATAGAAATTAATGACACTTGGTCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTATCCT	---
L18877	69	T C	TGAGTCTGAGCAGAGTTGCAGCCAGGCCAGTGGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC C[T/C]ATCCATTAGTTCCACTGCCTCGTGTGACATGAGGCCCATTCCTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTCCTGTTGGA ATTGTTCAAATGTT	---
L31848	36	T C	GCTATTTTACATATCCCAAGCCCTTTAGGGCTACAG[T/C]CTCTTCTTGTCCTGGACCCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAGAAGAAAAAGGCTTTGGGCCTGGTGGTGGCCATAGGCCTGTAATCGT AGCGGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGAGTTGAGACAAACCTGGGCAAT GT	---
L38517	137	G C	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGCCCTGGAAGGAGCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAAGACTTGACTGGGCAACACCAGCGTCCCCCAC CC[G/C]CGCTGGTGTGGTGTCATAGAGCTGCAAGCTGAGCTGCGAGGGGATGGTGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG	---
L39059	123	T G	ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTTTCTTTGTATTTGTATATT[T/G]CGCCTGA AGATCATCCCGCCAAGGCAGGCTGGAGGTGCCGGTGGCCTGTGTTGCTGGGCCTTAGTCTGTGTCTGG GAG	---
L41268d	173	G A	CAAAGTTGTCTCCTGCCCATGAGCACCACCAGTCAGGCCTTGAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTTGCCAGTCCAATGTACCAGCAGCTGGAATCGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCCTCACCACCAAAATCTGAAC[G/A]TGCCTCTCCCTCCCTTGCTTACAAATGTCT AAGGT	---

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L48728b	111	T	C	AAGTGAACAGAGAAAGCAAAGATGGATTGTGTTCCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTGGTTACTTTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGGATTTTTAGCCCAATGCTCCAAAAACTCATCCTGTACCTTGGAGATCCA GTC
M18079	52	G	A	GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTATTTCACC CCATCAAGTATAAAGGTTACTGATTGGTCCTTTATAAACATTGGTATATTCCATTCATGCCAA AGCAAAAGAAGTAAAAGCTAA
M19169	113	T	C	TAGGGATCTGTGCCAGGCCATTCGCACCACCACCACCCCCTGTAGTGCTCCCACCCC TGGACTGGTGGCCCCACCCTGCGGGGAGGCCTCCCCATGTGCCTG[T/C]GCCAAGAGACAGAGAG AAGGCTGCAGGAGTCCTTTGTTGCTCAGCAGGGCGTCCGCCCCTTCCTCCTCCGCTTCTAATA GC
M21539	114	T	G	TCACCTGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCCTTAGCCTGTGATCTGCCCATGAGTCCCGACAGCAAAAT[T/G]TTCCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAGGAAGTCCTCAGCTGTACCGGCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173	A	G	CCTAGCATTATTTTCTGGCCCCATTATTATCATATCCCTTTCTCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTGAATTATTCCCTGACTTC CTGATTTTTTTCTTTCTCA[A/G]TGTTACCTACTAAGA[A/G]GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A	G	CCTAGCATTATTTTCTGGCCCCATTATTATCATATCCCTTTTCTCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTGAATTATTTCCCTGACTTC CTGATTTTTTTCTTTCTCTC[C/G]CAAATGTTTCTCCTCTCACC TAATTCCTCAGTAA
M26041a	45	C	G	CCTAGCATTATTTTCTGGCCCCATTATTATCATATCCCTTTTCTCTC[C/G]CAAATGTTTCTCCTCTCACC TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTATTTCCCTGAC TTCCTGATTTTTTTCTTTCTCAAGTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G	C	TAAGGCAGCTGTCAGGAGGCCCAGTCAGTCACAGTCCAGCAATTCCACAACCACCTTGAC[G/C]AATGCT TGCCAAGCTGTTTTAAAGCCAAGAACACACCCTTTCTTGTTCCAAATTAACTCTTAGAAGAAACCCCA CAAATAAAGCAATTCAATC
M81695	34	G	A	ACTTACTTACCCTCACCTGTCAGGCTCAGGGGA[G/A]GAACCACTGCCACCACCGCACCGAGAGAGGCTGGG ATGGGGCCTGCTTCCTGTCTTTGGGAGAAACGTCTTGCTTGGGAGAAACGTCTTGTTGTCA[G]GTTC CAACTGGAAACCCTTAGGACAGGGTCCCTGCTGTGTCCCCAAAAGGAGCTTGCCCTGTGCTGACTTGCAATTTCTACC T

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U06641d	166	C	T	---	CTCCTCCTTATTCAGCATGGAGGGTTAAATGGAGGATCTCCTTTCCTGTGACAAAACATCTTTCACAACTTACCTTGTTAAGACAATTTAAAAAAGATCTTTTCACAACTTACCTTGTTAAGACAAATTTATTTTCCAGGCTATTAATACGTACTTTAG[C/T]TGGAATTATTCTATGTCAATGATTTTTAAGCTATGAAAATACAATGGGGGA
U09607	39	T	C	---	GAGGCCTTATGGAGGGTCCTCTACTTCAGGAACACCCCCA[T/C]GACATTGCATTGGGGGGGCTCCGTGGCCTGTGAGAATAGCCTGTGGCCTTTGCAATTGTTAAGGTTCAAGACAGATGGGCATATGTGTCAGTGGGGCTCTCTGAGTCCTGGCCCAAAGAAGCAAGGAACCAAATTTAAGACTCTCGCATCTTCCCAACCCCTTA
U09608	82	T	C	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTCGGGAAAGTCTGGTCC[T/C]ACATCTGCCCGGCCCTTCCCAGCCCTCCCCAGCCCTCCCTCTCTGTTCTTCATTCATTCAACAAATTTGGC
U10694	20	C	G	---	GTGACATGAGGCCCATTCTT[C/G]GCTCTCGTGTGTTGAAGAGAGCAATCAGTGTTCTCAGTGGCAGTGGGTGGAAGTGAGCACACTGTATGTCATCTCGGGTTCCTGTCTATTGGGTGATTGGAGATTTATCCTTGCTCCCTTTTGGAATTGTTCAAATGTTCTTTAATGGTCAGTTAATGAACTTCACCATGCGAAGTTAATGAATGACAGTA
U13877b	162	T	C	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAACCTCTTTGTTCAGAAATTTCTCCATGGAGTAACAATATCTAGGTGGGAGGATTAGTGAAGTTACATGTAAAGCACAGAGAACACAGCCAAGAGAT[T/C]TTACCGTGGTCTTACTAAAGTACATATCCTAACTTGGGGTTTACCTTCAGCA
U15555	187	T	C	---	TTTCTGTCCACTTTCACCTGGTTTTAATGATGCCAGCCAGTCAATAATAGTAGAGGAATCAGTCAAGCAAAAATGCTTTGGAAGAATTAAATAAGCAATGCTGAACATCAGGAATTGTAGATATCCGTACAGAGAGTTCCAGTGAAATTTTATGAGTCCACGACCCCTTTCTAAGCAGTCTGGTCCATG[T/C]TGGTCTCATACCTCATATGCAGGATTCATTCA
U17077	122	T	C	---	TCCAATTATTGGTCCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACTAAAACGTCCACGCGGATTAACAGAACGTCCTTGCAGACTGAGCGATGACGACCACAC[T/C]TGTTTGGACATTTAAATTCACTCTGCTGAATAGGAGGGAAGCTTTTCTTTTCCTGGGAAAACAACTGTCTCTTGGAATTA
U18543	58	T	C	---	GCACACATGCAGAATAGACTCAGCCTATGTCCTGATTCCAGCTGGGTAGTTCTAGAAACTT[T/C]AGAAAGCTCCATCTTTAATGTTTTATTTGTTATGTCCCCCTCCCGGCTTCCCACCTAAATTTAGAGCTTTAAAAGATGCACTGCCCAAATAGGACACACGATGTGGTGTTGATTAGCAAGTTGATTAGCAATTAGGCACTTCCAAGGCTTTAGTAGAGAGAGCC

ID	Pos				Sequence
U25975b	164	C	A	---	TCACTGCTGTGGCCTCATACTCTTTTTCCATTTCTACAAGAGAGCCTTTAGTATATGAAAATTATT ACTCTTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAAAGAAAGAAGCAAATGACTATTCTCTG AAGACAACCAAGAGAGAAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C	G	---	TCACTGCTGTGGCCTCATACTCTTTTTCCATTTCTACAAGAGAGCCTTTAGTATATGAAAATTATT ACTCTTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAAAGAAAGAAGCAAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A	G	---	CAGGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTAGGGGTGTTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAGAAAAATT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCCCACCAACAAAA TCC
U28413	29	C	T	---	ATTCCTGACAGCTAAATTAGCCCCTAAAATG[C/T]GGGTAATATATTTTTCCTCATGTTTTAAAATGAGGTT AATATTTGCATAAAAATCCTAAAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCCTTGATCC CAGATGTTGTGGCCTTCTGGGAAAGCCCTCATTGTCTACAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89	A	G	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATTCCCACGTTAGCCAA[A/G]TTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACTGCCCACAGTTGAACACAAGT GCTGTCA
U30884a	34	A	G	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTCCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACTGCCCACAGTTGAACACAAGT GCTGTCA
U31216b	78	A	G	---	GGGACAGCACATATGTGGCACCGCCTCCTGTGCACGTGAAGACCATGAGACGGCCTGCAACCAAACA GCCGTCATCAA[A/G]CCCCTCCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCTTTACACACGTAGAGGAGGAGGATGCCCAGCCGGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G	A	---	GGGACAGCACATATGTGGCACCGCCTCCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAACA GCC[G/A]TCATCAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCTTTACACACGTAGAGGAGGAGGATGCCCAGCCGGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT

ID	Pos	Allele	Sequence
U31416c	76	G A	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTTGCTTACAAATGTCTAGGTCCCACTGCCTGCT GGAAAGAAAACACACTCCTTTGCTTAGCCCACAGTTCTCCATTCACTTGACCCGTCGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68	C T	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCCTCACGCGCCACAAATCTGGTGCCTCTCTCTTGCTTACAAATGTCTAGGTCCCCACTGCCTGCTG GAAAGAAAACACACTCCTTTGCTTAGCCCACAGTTCTCCATTCACTTGACCCGTCGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U375519a	78	C T	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCCTCC AGACCGCAGG[C/T]TCCCCCAGCCTCAGGTTGCTGGAGCTGTGTCACATGACTCCTGCCTGCCAGG GCTGCAAAGCAAGGTCTTGCTTCATCTGGGGGACGGCTGCTCGCGAGAGAGGCCGAGAGGCCGCAGAAC ATGCCAGGTGTCC
U37690	54	A G	GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCCATGGGCCCTGAGCGTCCT[A/G]CCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGCCAGTGTGTTGTATCCCATACCCCACT CTGGAAGGAAACCATCCAGTAAAGGTCTTT
V00540	39	T C	TGAAACCGTTTCAACATGGAAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTCAGATCTTT TCAGGAGTGTAAGGAAACATCATGTTACCTGTGCAGGCACTAGTCCTTTACAGATGACCATGCTGAT A
X15943	106	A T	TCAAGAAGGTGACTGCGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGGTAA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTAAAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCCAGTAGCTAAGACCCTAGAATTTGGATTCATCTCTGTTTTTTCATGTCTCTCCTT GTAACCCTGAGATCATCAG
X52011b	148	C T	AGGAAGAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTAACATTTAGGA ACCCGAGACCGAAAAGTTGCTGAAAGGGAAGGAGGACACATTCACAAGAAAAGTTGCGAAAATTGCG AAATCTGTTTGTGCA[C/T]GCTCAAATGAAAACGCCCTTTGCGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118	A C	AGGAAGAATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTAACATTTAGGA ACCCGAGACCGAAAAGTTGCTGAACGGGAAGGAGGACACATTCACAAAGAAAACGCCCTTTCGGCTTTAT TTGGGCTTTATTTTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

Accession	Position	Allele 1	Allele 2	Sequence
X54741	24	A	G	CAGGCCCACCTGTCTTCTCTCCCAC[A/G]TGCACAGCTTCCTGAGTCACCCCTCTGTCCAGCCAGCTCCTGCACAAATGGAACTCCCCAGGGCCTCCAGGACTGGGCCTTGCCAGGCTTGTCAAATAGCAAGGCCAGGGCACAGCTGGGAGACGATCTTGCTGGCAGGGCCTGGCCTTGTCCCCAGCCCACCTGGCCCCTTCTCCAGCAAGCAGTGC
X54869	99	A	G	AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAAATAGAAATATTATGATTGCATAAATCTGAAAATGAATTATGTTATTTGCTCT[A/G]ATACAAAAATTCTAAATCAATTATTGAAATAGGATGCACACAATTACTAAAGTACAGACATCCTAGCATTTGTGTCGGGCTCATTTGCTCAACATGGTA
X66924	147	G	A	GCCGGTGTCCTGACACCTCCAGAACGCAGGTGCTGGCGGCCGTTCTGCCCTGCGGCACCCCGGAACCTCTCCTGCCGGAAGCCGGACGGGCAGGGATGGGCCCCAACTTCGCCCTGCCCACTTGACTTCACCAAATCCCTTCCTGGAGACT[G/A]AACCTGGTGTCTGCAGGAGCTGGCTGGTGCCTGAAGGACCAGA
X78932	62	T	G	GAAATGTGAAGAATGTGACAAAGCCTTTAAGCGGTTGTCACACTTGATTGTATATAAGATAA[T/G]TCATACTGGGAGAAAACTCCCAGAAGTGTGACAAAATGTGACAAAACATTTAATTCTCATACCTTATTGCACAGGAAAGCATTTATACTTGAGAAAAATTGTATAAAGAATGGAAAAGTCATTAATATCTGCTCATATCTTAACATCAGCGAGTT
X80026	25	T	C	CTCAAACCCATAAACCTCAACCACATC[T/C]TATCCTCCACCCCACCATCCACCTCCATCCCAACCCATCCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAACCCATCCCCAAGCCCTCATCCTCATCCCCAACTGCAGCCCCAAACCCAACCCAGGCCATCCCCAAGCCAAACTCAACACCATCC
X80197b	99	G	C	ACCCCAACTCAAGTCCCAGGCCCCAGGCCATCTTTCCTGCCCATCCAGTCCAGGCGCCTGGAGCAAGTGCTCAGCTACTTCTCCT[G/C]CACTTTGAAAGACCCCTCCCCACTCCTGGCCTCACATTTCTGTGTGATCCCCACCCCAACTCCCAGCCTCTGCCTTGCTTGGCCCATCCAGTCC
X80197a	28	A	G	ACCCCAACTCAAGTCCCAGGCCCCAGGC[A/G]TCTTTCCTGCCCATCCAGTCCAGTACTTCTCCTGCCCACTTGAAAGACCCCTCCCCACTCCTGGCCTCACATTTCTGTGTGATCCCCACCCCAACTCCCAGTGGGAAAGGCCACCCTAGAAAG
X85106	150	G	A	GGCACCCAGAGTGACCACAAGTCCAGCAGGGAGGGAGCCGCCGCCTGCCGTGTCCGCCTGCGGTTTTTTTTTCAGCCCCGGAGAGGTCCTGACCTGGGGCTTCTCCAAGCTGGCCACGCCCGTGCGCCACCCTTCACCTGCGTGCGCCCGTGCGAGGCGCCGGGGGGCTTCTTTCAGAGC
X87160	128	T	G	ACCACCAGCCATGGTCTAAGGACATGGATCGGGTGCCCCCAGCAGTGTGCACAGGGACCCTGCCCCCACTCTGGCTTTTCAGATACTCTGACCAAAAAGCTGCTTTAAACCGCAAGATGGGCGC[T/G]GGGCATGGCGCAGGAGGAGCCCATCGGGTACTACGCAGCAACACTGTCCAGCTGTCCAGGCTGCAGATAAATCCCGGGA

X87344	34	C T	CATCCCAAGGCACTGGTGGTGACTCTGCTTCCTG[C/T]ACTGACCCAGAGCCTCTGCCTGTGCACTGC AAGCTGTGTCTACTCAGGCCCCAAGGGGACTCTCTGTTCCATTCTCCCCCCACAGACCTGTCAAGAG AAGCATGACAAACAAAATCATTTACCGACTTAGTGCTTTTTT
X87838	179	G T	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCCTATGGGAACAATTGA AGTAAACTTTTGTTCTGGTCCTTTTGGTCGAGGAGTAACATACAAATGATTTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAGAATGGATCACAAGATGGAATTTA[G/T]CAAACCCTAGCCTTGCTT GTTAAAATT
Z14138	81	A G	GTTCTGCTGCCTCTACACAGGGCGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC[A/G]TGAATGTGCCTCCAAGCGGCCCTGTGTGTTGACATGTGAAGCTATTTGAT ATGCACCAGGTCTCAAGTTCTCATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191	A C	TAATCCTCACCATTCCTCAGGTATAAGTTCTATAAAACAGGCTTGGAATCTGGGTAATTAAAAACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTCATACGTTCTTTCAAAGTGTGGGATAGCTATTGCAGCTTAAAGAGC[A/C]CAGGTTC CAGTACTGGTTTCCAA
Z23091	159	G A	AGAACCTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGGCTGTCTTGCTCTCCTCCTCCCCCTCCC CACTCCTCCTCTCTCTCCTCTCACTGCCACCCGCCTTCCTCCTCCTCCTCCCCCGTCTCTGGAAA CTCTGTGCTGCTTCATTCTCAG[G/A]GGCCCGCAACCCCTCCTCTCGTGTCCCGTCTCTGTCTCTGGAAA CTGAGCTTGACGTTG
11595b	125	A G	GTTGGCATTGTTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAAACCTGACCTGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTCTACCTTGTCTTTGTTGTGAAAGGAGTGGTTCCCATGACTGTTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
11595	125	A G	GTTGGCATTGTTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAAACCTGACCTGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTCTACCTTGTCTTTGTTGTGAAAGGAGTGGTTCCCATGACTGTTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
1241	131	G T	TATATCACATTAGTATGTCACTGCCATGCCATGTAAATAAGAAATAAGAACACTTTGAA TGGTCTTGTCCTTTCAATAAAAGAGTGACATGATTGAACATGTGTTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGTTTAGGATGAAGATGAAGAGAGATTAAGGAAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAAAATAGGAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAGAGAAAG

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1282	130	C	T	GTGCGGATCACCACTACAGTCTAATTTCAGATGTTTCATTACCCCTAAAAGAAATCTTGTACCCATTA GCAATTATTCCTCCATTCCTGCCCTCACCCCCAGGCCCTACTCTTTATCGCTATAGATTTGCC[C/T]ACT TGACATATCATACACATGGAGCCATACATATGTGCCCTTCATGATTGGCTTCTTCACTGAGAATA ATGTTTTCAAGGT
6810	68	C	T	AGTATCACACATACTTAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTT A[C/T]AGAAGCATTTTAATTTACAACACAAAGCTCAAACGAACCTACAATAAGTCTAGTAGTCTG TTTACGTGCCAAAGGGATAAGGCTGAACAATAAATTAAACCCTTTAAAAATGTCTATGAACAAGTACAA TTTTCTTTTGAGTTCTGCAGAGCAATGACCACTAAGAAATATTTTAAAGGC
6817	118	A	C	CCAAGTACAATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTGCTTTTTGTAATCCAGTTAAGACCA TCAGCAGTATACAACATCATCAACTCAACTCAACATGTAGCTGCAGGGTAAC[A/C]TGTGGATACCCTG TGTGCTCTACTGGCCTCCAAAGGCATTCAGGGGATCATCAAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGCGCGGCCTGTGCAGATCGGCGCTTTTGGGTTGTCTTAG
6819b	212	C		CCATTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATCATGTCA CCCTGAATGCCAGCAATACCTGACTTTTCACACGCAGGAAGCCTAGTAAAAGCCCGTCAGTAGT ACACATTTCTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTGCTTTAGCAAA CAGCAATAACTTTGTGTTCCTATATGACACCTAATATCCA
6819a	166	G	T	CCATTTATTTTCTCTAAATTTTAAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATCATGTCA CCCTGAATGCCAGCAATACCTGACTTTTCACACGCGGAAGCCTAGTAAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATTTTGCTTTAGC AAACAGCAATAACTTTTGTGTTCCTATATGACACCTAATATCCA
681xx	39	A	G	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCACGAATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGT TTAACAAAGAAATGAAACGTCTAGG
6972b	149	G	T	AGGATTCCCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTGGTTGGTAAACTATTGATTATTGC CACAATTTCAGA[G/T]CCTGTTATTGGTCTATTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122	A	G	AGGATTCCCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTA TTGCCCACAATTTCAGAGATTCTATTGGTCTATTCAGAGATTCAACTTCTCTTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210	A C	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTATGTGAGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208	A T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTATGTGAGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCC[G/T]ATTTTCCT CAATGC[A/T]GA
7598i	192	G T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTATGTGAGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCC[G/T]ATTTT CCTCAATGCAGA
7598h	144	C T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598g	142	C T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598f	120	A G	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCTT TTAATATTTGATCCCATTATGTGAGAGAGATTTCCTGATATGTTATTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598e	83	C T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCT TTAATATTTGATCCCATTATGTGAGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598d	77	C T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGC[C/T]GCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCT TTAATATTTGATCCCATTATGTGAGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA

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7598c	56	A	G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAGAGACACCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAAATATTTCTTGAGGATGCCT TTAATATTTGATCCCATTATGTGAGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598b	47	C	G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAGAGACA[C/G]CAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAAATATTTCTTGAGGATGCCT TTAATATTTGATCCCATTATGTGAGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598a	30	A	G	AAAGGTAAATCAAAGTTCCCTCTATAAATT[A/G]TGATTTACAAAGAGACACCCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAAATATTTCTTGAGGATGCCT TTAATATTTGATCCCATTATGTGAGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7998c	116	A	T	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTAATGAATGGGTGTAGTCCTATCTTCTCAAGGTCCCCAAATA[A/T]CCTTGAGGTTCCT
7998b	94	A	C	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGTAGTCCTA[A/C]TCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
7998a	75	A	T	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTT[A/T]ATGAATGGGTGTAGTCCTATCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
8071	119	A	G	AAATACAGAATTTATTTAGAAACTGTTTAAAGTAGAAAAAAACCCTGTCAAGAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAACAAAGTCTAAAAGGCC[A/G]CAAAAGAGA AATAGCACCACTGTCATTGAACAATGGCTAGTTACTTGCATTTTTGGCATTGTTAATCACTGAATC TGGGTTTCCTCTCTGAATTCCACAGAGCATGCCACTACCACAACATTTTTATCAT
8467b	93	C	T	AAGGCTTCCTCTAAACATCAGTCCTACGGAGAAATCTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCATCCCGAACTCCCTCAGAGGAGCAAGCAAGCAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAAGGAAAAATTACTG
8467a	70	A	G	AAGGCTTCCTCTAAACATCAGTCCTACGGAGAAATCTGGGAAATCCTGGATATTTGGCTTATCACTT TG[A/G]CGCAAAATCCACTTTGCTGTAACGGTCATCCCGAACTCCCTCAGAGGAGCAAGCAAGCAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGTATTAAGGAAAAATTACTG
8498	84	C	T	AGGGGTTCAGGGGTTGGTTTAAATCAGGCTGCACACCTTTCAAATCAAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACTTCATTCATTAAAATGAAAAAAATTGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAATTAACATTAGTCTTTAAAATAAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCCTCCTCAATACAGAACCAGGAATGTAATTTCCTAACTCAG

Name	Pos			Sequence
WI-18562	29	G	A ---	CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAGCTTCTCTATTTCACATAGCTTAGTTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATTTAGCATTAATCAGAAACGA
WI-18618	51	A	C ---	ATAGCAGACTTTTAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCGTTACAATGAAGAAATGGTTTCCTTTGCGATGCAAAGTATAATTGTAAACCACAGTGCTCGCACAGTTCAC
WI-18683	22	C	T ---	TAAGCTGTTCAGGACTGGACTC[C/T]GGTCCCTTTATTGAGACTGACACAGGCCAGTGGGTCCACCCAAACAAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75	G	A ---	GACTTTGGTGATTTAATTGCTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTGTTCTTTACTACA[G/A]CCGGAGTGGTAAATACTACCTGCCAACAAACACGGGCATCCACTCTGTCTTCAATGCCCTCTTCCGTGAGAC
WI-18563	94	A	G ---	AAATAAAGTTTATTGGCACACAGCCAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAATACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T	A ---	GTCCTATTCAATTAGCTAGACACCCATTTCATTCGTCGTTTAATGGCTACATTGTTTTTCATTGTGAGAC[T/A]GTGCCATAATTATTTAATCAGTGCCATATTGAAAGACATTGGATCGTTCCCAG
WI-18723f	94	G	A ---	AACTTTATTTGATCTGACGATCAGCGGATTAGTTCTCATCCACATTAGTTTATTTGGTGAATCTTATTCCTTGGTAACAGGTACATAGGTAACCAAA[G/A]TATATAGCTTATTTGGTGAATCTTATCATCCT
WI-18723e	71	T	C ---	AACTTTATTTGATCTGACGATCAGCGGATTAGTTCTCATCCACATTAGTTTATTTGGTGAATCTTATTCCTTGG[T/C]AACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTATCATCCT
WI-18723c	96	A	G ---	TTTATTACAATATTTAGGTGGCACACAAGAAGTAAAACTCGAAATATAGACTTTGCAACTCAGCCAGAAGTAAAAACTGAAATA
WI-18619	44	G	A ---	TTATTCACAAAAAGTGATATTGCGAGAGGGTCTGGGGGCTGTACATGGGCAGGGGCTTGGTGAGCTTTGTACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTTAATAAAAAAATAATGGAGCTACAACCACCCC
WI-18715	76	G	A ---	GTAAATAAAGTTTTATTGGCACAGCCACGCTCGTTCATTCATATGCCATTGACATCTGCTGTGCCCTACACAGCAGGGTGGGGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTAAAGCAGTGGTCCCCAACCTTCTGTGGTCCCCGTG
WI-18535	107	G	A ---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCCTCACTTACTAGTTTTCAGTTCTGGGCAGGTGACTTCATCTCTTCGAACTTCAGTTTCTTCATAAGATGGAAA[G/A]TTGCTATACCTTACCTACCTCGTAAAAGTCTGATGAGGAAAAGATTAACTAATAGATGCATAGCATTAACAGAGTGCATAGCATACACTGTTT
D17525	107	C	T ---	TCAATAAATGCACCTTAGCAGAGAAGGTCGATGTGTCTACCAGGCAGAGCAAG

DWU-133c	313	A	G	TAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATGTTCAGTTTTTGAATTTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTAAAGATATGATTAGACT
DWU-133b	236	T	C	TAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATGTTCAGTTTTTGAATTTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTT[T/C]TAAAGATATGATTA
DWU-133a	199	C	T	TAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAGTTTTTGAATTTAATAGTAA[C/T]TCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTA
DWU-36	102	C	T	ATGAGATCCTTTAAATCCTTCCATGAAACGTTTGTGTGGTGGCACCTCCTACGTCAAACATGAAGTG TGTTCCTCCAGTGCATCTGGGAAGATTTCTACC[C/T]GACCAACAGTTCCTTCCAGCTTCCATTTGCC CCTCATTTATCCCTCAACCCCCAGCCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGAATTCATGTGAATATAAAGAT
DWU-387	169	G	T	GTGTATAAAAATGCAACTGTTGATTTCCTCCAACATGGCTCACAAATTCTATCCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTAAAACTGCACTGCCAACAGTTCACTCACTTCATATATAAAGCATTATTTTA CTCTTTTGAGGTGAATATATAATTTATATTACAAATG[G/T]AAAAGCTTCTTTAATACTAAGTATTTTTCA GGTCTTCACCAAGTATCAAAGTAATAAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172			ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAACTGTCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAAAAATCACTGTAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTTTCATTTTGTTCTCAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTGTTTAG GCCTTCTTTCTTCTTACAATGAAGAGATGAATTCTTCTAGTTTATGGTTA
DWU-447	85	A	G	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAACTGTCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAAA[A/G]ATCACTGTAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAAT CAACCATTATTTTTCATTTTGTTCTCAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTG TTAGGCCTTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C	G	GTAAAATTCAGTTTTTCCAGTTCCTTCTTTTGTGCTGCTTCTCAATTAGCGTTTAAGGTGTGAG[C/G]AT AAATCAACTGTCCATCGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCCATGAGTAGTGGGCTATGCA GGAGCTTCTGCTGGGGAGATTTTTTT

					Sequence
DWU-505	67	A	T	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATTCTATCACCATACAAAAATTA[A/T]GCAGTATTATGTTTAAAGCACAGGTACCGAAAACTGTGAAAAGTCTGAATTTATGGGTTCTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTGAAGATGGATTAACTTTTGACTTGAGCTTTAAACTTTAA
DWU-512	131	A	G	---	AAAATCCAGGCATTCGAATCTGTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACTTATTAAAGAGCTTCCACAGTGAAGATGGAGAAGGTGAACTGCTTGAATATTCCAGATGTGTTTGGTC[A/G]TGCGTATGGCAGTGAGCAGGTATGTGTTTGCTTGCTTTGCTCACTGAAAATTAAATTGCTATCAAGAGCAAACTATGAACGGTTTTTATTCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A	C	---	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATTCTTTCAGCTTGTTTCTATACTGTTTGTAATATACAGTTTTGTAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACACCCAATTTAAAAAATAACAACATATCTTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAATTCCACCAGGATTAATCTCTAAAATTCTAGTCTCTGATTTGC
DWU-59	94	C	T	---	CATTTCTTTGTGAAAGGTAATGGACTCACAAGGGGAAGAAACATGCTGAGAATGGAAAGTCTACCGGCCCTTCTTTGTGAACGTCACATTGGC[C/T]GAGCCGTGTCCAGGTGGCCAGACTCGTTTTGGTAGTTTGTTTTAACTTCCAAGGTGGTTTTTACTTCTGATAGCCGGTGATTTCCCTCCTAGCAGACATGCCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C		---	CTTGATCATGGGGTGGAATTTGTGTATCTGGGCTTCATGGGATGCATAAAAATTTTCCAGTTGGTAAGCAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAAGGCA
WI-19856b	63	C	T	---	CACACTGGCATCTAGGCCTTCGCCTGCATTGCAGAAGGAGAGCCAGGTCCCCCTCCTGGAGAA[C/T]GCTGCGGTTCCCCAGCCCCACACGGCTTTGCACCACAGGTGTTGAGGCAGGAGGTGGGTAAGACGTAGCTGTAGACCCAAAGCAACCACCAGCCTGGACCCTGCGGGAGGAGCACATCATTAGACAAGAACACATCCTACATAATAAAAGTAGTGTGGTCATCCATCATTAGACAAGAACACATCCTACATAATAAAAGT
WI-18014	40	A	G	---	TCCATTTACATTGGTGGCATTTGTTGTTGATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGTGTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAAGTGGCTTCTA
WI-18036b	97	T	A	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACTTCTAGAAATACAAAGAGAACATGATAAAATCTGATCAGGTGGAAAATTTTAATTCTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATATTAGGGATCTGAAGG
WI-18036a	27	T	C	---	TTCCAATGTAAGAGTCAAGTCAAGTACCAAGT[T/C]AAACTTCTAGAAATACAAAGAGAACATGATAAAATCTGATCAGGTGAAAATTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATATTAGGGATCTGAAGG
WI-18046	72	C	T	---	TGTAAGGTGACTTCTATAAGCTTCCTAAACTTGTCAAACTTCATTTACTGAGATTATTTCAGGCCAATGTGT[C/T]GGGTCTGAGATTGATTATCAGCTGGGTAAGTTAACCTGTTCCTGTTTCA

ID	Pos			Sequence
WI-18063	105	G	A	AGGCTTAAACTGATAACAATTGCCTTTAATCACATACACAAAAACTCTGCCACTTCATTCCTTCCTTC CCATGTTTTCTGATTTGATGTAAACTTAAAATTGT[G/A]TCCTTTAACAATATACTGGTCCAGTGTGCA
WI-18078	86	A	T	AGTTGAAAGATCAGAGAGGTTATGGTTGGTGAGTAGCTGAACTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTCAGCATCAG[A/A]GTCCACTAGCCAAGTTGATCTCTGCAGTATCTCACATGTGGT
WI-18091	90	T	C	CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTCCTTTGTTAATTCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTGACT[T/C]GGGCCCTTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18119	38	T	C	GCAATCTGTAACAGTTTGGTAGTGGTATTACAGAGGA[T/C]TGTAAAATGGATTGGAGTACTTAC CACTATTTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAATTTGGTTCTT
WI-18142	66	T	G	TTCAAGATAATTACAATTGGAAGGGGACCAATAATTCCCACTTTTTAATCGAAAATAATCTATATAC[T/G]CCCAATAAAACTCACAGTAAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T	C	GCATAGGGGTTGAGGGGTGTACAAGAGGAGAACCAGATTCAGTCCATGCCTGGAGGTTAGTCTGGGGG G[T/C]CGGCGGGGATGGACACACAGCAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G	T	TCAATCTGAAAACTTGCTGTAAGCCACCAGCATGGGT[G/T]GGGGAGGTGATTATGGCTGGGGAAGATG GGCCACTCACCCGACAGCAGCATCTAGCACCACAGTGAGGACGTTGAGGGTGGCAGAGGGCTTT
WI-18245	115	G	A	ACAGATGTCAGTTGTTTGAAATTGGCCCATTAAAGTATGGGGCTTTCTTGTTAAAAGTCATTCCAAA AGGCTTGGCAAGAGGTTGCTATACACGGAGGAGGACAGAGAAACATGA[G/A]CTGGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26	G	A	GATTTGAAGGGATTGCTTTATTTAAC[G/A]TGAAAAAGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAAATACTCCCAATTGTGAGAAGTGAAAGATTG
WI-18268	88	C	T	TAGGAGGGAAAAGGAGAGGTGGGCCTGCCTGGGCCCTGACAATGGAAAACGGGGTGGTTCCAAGC TTCCTTACTTCCCCCATAGAT[C/T]CCTGACAATGTGCTGCAGAAGCCTCCAACCTGGAAC
WI-18299f	107	C	A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTTT ATCTATTTGGGTCTGAGAATTCCACAATTTTGCCAATTATTGACATATTCTG[C/A]TTTGCCAATTATTGACATATTCTG CAG
WI-18299e	101	A	G	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTGG[A/G]TCTGAGAATTCTTTGCCAATTATTGACATATTCTG CAG
WI-18299d	77	G	A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTG[G/A]GTCTGAGAATTCCACAATTTTGCCAATTATTGACATATTCTG CAG
WI-18299c	67	T	G	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTT[T/G]ATCTATTTGGGTCTGAGAATTCTTTGCCAATTATTGACATATTCTG CAG

WI-18299b	52	G	A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTG[G/A]TTTGCCAATTTT TTTATCTATTGGGTCTGAGAAATTCCACAATTTTGAAGAATTCTTTGCCAATTATTGACATATTCTG CAG
WI-18299a	48	C	T	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAA[C/T]TTGGTTTGCCAATTTT TTTATCTATTGGGTCTGAGAAATTCCACAATTTTGAAGAATTCTTTGCCAATTATTGACATATTCTG CAG
WI-18307	76	G	A	TCAACTTGTACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C	T	TTTGGTATGAAAATCTTTCTGACATTTACCAATCATCACTTAAACTCCGGGGGTGGGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAGTG
WI-18350	48	T	C	ATGAAAGTCACTTCAATCATAAGGGTCAAGAGAAAGAATGTTTCAGA[T/C]TAAATCTATGAAAA GGTGTGTATCTGCTTGCAATTTAAGAAACAACAACAAGTCA
WI-18395	77	G	C	TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAATTCCTGGAAATTTGAAGAGAATAAATTG ATTATTCAAG[G/C]TGTGCATTGGTTTATACATATCTCCTCTTAATGCAAAGCTATG
WI-18398	62	G	T	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAAAAAAGAAAAACAACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATAATTCAAAACAAGCAGCAGAATTGGAGGATAAATTTGTT
WI-18396	21	C	A	CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTTCGCTCTTTCTAAAATTAAAGAAAAGCAATGGAATT TTAAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGTACAAGTC AATGAAAA
WI-18409a	20	C	A	AAGATGGGAAAGAGGAAATC[C/A]TTTTCTTACTAGAGATTTTTTCCCTTTAATCCTTTTCAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAGCTCTGGGGCCCCAGTCCCCAAGTGCTA
WI-18442	62	C	T	AAAAAGGAAAAGAAAAGGATGGAGTGAGTAAGACAGAGAGAGGAACAAAATAAGTTTCTGG[C/T] JTTGGCTAATCTGGGTGATCAGGTGGACACTATTATCCCAGAGGAAACACAGAGAAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38	G	A	TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCCTCATATTTCCAACCA
WI-18489	102	A	C	ATATAAAGCTGGAGACTGTGGAGGGTGAGAGGCAGTGGGGACTAGCTGTTGAAGAGAATGTAGC AGTAGTAAAGATGAAAGACTGCAAAACA[A/C]GGTTATGGCAATGAAGGTGAAAGAAA AGGCCATATAAA
EST5b	93	A	---	CTGGTGGGGAGGGAAACAAATTGTGTATATTCATACAATGAAAACTCTTCAGAAATAAGAAGGAA CAAACCACTGAATCACACAACACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCATTCA TAAGAATACACAGTACAT

Name	Pos				Sequence
EST5	93	A	--	:::	CTGGTGGGGAGGAGGAAACAAATTGTGGTATATTCATACAATGGAAAAACTCTTCAGAAATAAGAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCATTCA TAAGAATACACAGTACAT
EST6	48	C	--	:::	TTAGCTACTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAAGCTTTTCTTTTGCAACAAGACAAAGCCACATTTGCATTAGACAGAT
EST8	158	A	--	:::	GGACAGGAGACCTCTATTCCCGCCTGGTGCAGCAGCCCAGAGCTGATGGACTGAGGCCCAGGGATACTGGGCC CTCTTCTCAGGGGCGTCTCCAGGACCCAGAGCTGTTCCTGCTTGAGTTCCCTAGAGCTGTGTCGGCCA GATAGCTGTTCCTGAGTTGCAAGCACGATGGAGATTGGACACTGTGTGCTTTGGTGGGT
WI-18740c	104	G	T	:::	TCCTCATTGTTGGGGATGATGAGAAGAAAATGATTGGGAAAATTAAGTAACAACGACCTAGAAAGT GAGAACAATCTCATTTACCATCAGTATCCAGTAGTG[G/T]ATAATTCATTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96	C	G	:::	TCCTCATTGTTGGGGATGATGAGAAGAAAATGATTGGGAAAATTAAGTAACAACGACCTAGAAAGT GAGAACAATCTCATTTACCATCAGTATC[C/G]AGTAGTGGATAATTCATTTGATGGCTTCTATTTT TGGCCA
WI-18985a	105	C	T	:::	CCAAAGTCTCCTGTTCGCTCATAAAGAAGTTTTGGGGATGGGAGGAGAATCCAGACCCATCTTGGGGCA GCCAGGCCCCTGCCCTTCATTTTACAGAGGTAGCACAA[C/T]TTGATTCCAACACAAACCCCTTCCCC TTTTAAAATGATTTCTGTTCTAATGCCATAGATCAAAGGCCTCAGAAACCATTGTGTGTTCCTCTT TGAAGCAATGACAAGCACTTTACTTTCACGGTGGTTTTGTTTTTCTAT
WI-18746	114	G	A	:::	GCCAGCAGCTGAAGTCTCTTTTCTTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGGTGTACTTGACCGTTTTATATTACTT[G/A]TAAATATTCTT[G/A]TCCACATTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112i	212	G	A	:::	CCGTGTTCACACACACAATGGCAAGCAGCATAGTAGTGTCGCCTGGTTACGGCCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAAAACACAGATCAGTAGTGTCATCGATGCAACAACCAAGAAAACCGACGACAAA TCTTTTGCGAGATTTTCTTCTTAGTGGCTTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTTCAAACAGTTCCATACAACTGCTTTGCTCTAG
WI-19092	232	A	C	:::	TGGTGGCTGGCTAGCTAGTTTCTACAGAACACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAAACACTCTTCTTTCTTAGCCTTACTTGAATCTTGCCTATAATAAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCCTGAAATTTCATCTTGAATGTCTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC[A/C]ATGATTAGCCGTGTAACT
WI-19057i	175	G	A	:::	CCCATTTATTATAGGCCAGTGATGTGTCTCAAAGAGTAGAGGAGGGCTCTACTGGTCTTCAACTCCTTCA GTCTTCTGACGGCGGACTTACCGTGACAGCGGAAGTGGTATTGTACGTCCAGGCACGCAGCCACTG TCTTCATGCAGGAACCACCAGTGCCAGATCCCCACAGCTCG[G/A]TCTTCATCTTGTTTTGCCACA

ID	Pos			Sequence
WI-20103	168	C	T	TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCCAAATGATACAGGATAAACTGGGATGGGCTAGGATGGACAGGCTGTGGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAGTGGGCTTCCTGGGCGTGGAAGCTGGGTCCTCCCCCA[C/T]TTCATTCTGCTCAAAGCTTCTTGAAGGAGCTGGTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G	A	GCCTTACCCATTTGCACATATATACATGCCAGTGGCAACATATATCCACACTATAAACATACCACATTTATAAATCTTGTAAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCCAACATATACAAGAAAGTTAGCATACTTACCCCGTTTTCACTACATCAGAGGCAAAATAAGAAATCTTTTAAGAAAATCTCAAGACTGCTCATGGCAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A	G	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAAGAACGTTTTAGTCTTTTAAACTGAGTTAAAAAAAATAACAATGCAATTTTA[A/G]ACACTGTTTTGAAAACTTAAAAGTGCAGCAATA
WI-20613c	165	A	G	GTCCTCAAGGGGAGAGAAACTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACAGATACGTAGTAGTACATCTGTAGTATTAAAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAACAGCTCCTTAGAAGGCCAATATAAAGTTGGAA[A/G]AAAGGGAGGTTCCACGCAGCCAGTGGTGAGCTGC
WI-20613b	156	A	C	GTCCTCAAGGGGGAGAAACTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACAGATACGTAGTAGTACATCTGTAGTATTAAAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAACAGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAGGGAGGTTCCACGCAGCCAGTGGTGAGCTGC
WI-19984	47	A	G	CAGTAAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA[A/G]TATAAACATTAGAAAAGCAAAATTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGGTAGGCAAGAGAGTTTTCCCACACTGGAAAATGAAGGCAGTTTTCCAAATACTGTGAATTTACAAACATTGGGGGAAGG
WI-20122	135	T	C	GCCAGTTGGAATATGGCCTATACGAACCAAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATAATTGTTCCTTGGAACTCTGCACCGACTGCCATGCTCTGTGGGGACTTACACATTCAAGTTTGACAG[T/C]TGAAAAACCAACTGAGCTGCTTTTCCAAGAATGTTCGTTGTCCTTCAAATAGGAATTCCATGTTATTTCTTTCTTGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49	G	A	GAGTGCCATACCTTCTCCCCAGGCCTCTGCCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGCGTGGGCTCAGCAGGGCTGGTCACCTCCCATCCCGTAAGACCTCCTTCCCTTCCTCAGCAGGCCAAACATGGCCAGACTCCTT
WI-18959	123	G	A	AGCAGTGGCCTATTGCATCCCAAACCACGCCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGCACAGCTAATTCTACTCACAGTGCTTTAAGTGAAATGGTCGAGAAAGAGGCACC[G/A]GAAGCCGTCCTGGGCGCCTGGCAGTCGCCGGTGGCGGGGGATGGTTCTGTGCGGTGTTGAGATTCTCAAAGGGAGGAGCGAGCATGTCGTGGACACACAGACTATTTTGAGATTTCTTTTGCCTTTGCAACC

ID	Pos				Sequence
WI-20146	31	T	C	---	TGAGTCTCTGTGTAATTCATTGAGCAGTTAGC[T/C]CATTTGAGATAAAGTCAAATGCCAAACACTAGCTCTGTATTAATCCCATCATTACTGGTAAAGCCTCATTGAATGTGTGAATTCAATACAGGC
WI-18922	74	G	A	---	TAGGAATTGGTTTCACGCCTGAGGCAATTAGACACTTGGAAGATGGCATAACCTGTCTCACTGGACTTAAGC[G/A]TCTGGCTCTAATTCACAGTGCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCCAGAGGAGCCACCAGTTCTC
WI-18763b	53	A	G	---	TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[A/G]TATTTAGAAATGTACCATATTTTTTGTAAATTATTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAA
WI-18763a	38	A	G	---	TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGA[A/G]TGACGATGATGTGAATATTTAGAAATGTACCATATTTTTTGTAAATTATTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAA
WI-18771b	75	G	A	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGGAACAGAA[G/A]AAATAAACTGAGTTTAAGGGGGACTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A	G	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG[A/G]AGATGTTGGGAACAGAGAAGAAATAAACTGAGTTTAAGGGGGACTAAACTGCTGAATTCACCTGTGGA
WI-18820	70	T	C	---	GGGAAAAAATTTGAGACGGCAATACCAATACTTAGGATTTTGGTCTTGGTGTTGTATGAAATTCTGAGGCC[T/C]TGATTTAAATCTTTCATTGTATTGTGATTTCCTTTTAGGTATATTGCGCTAAGTGAAACTTGTCA
WI-18742b	51	C	T	---	ACAAAGTCCTGTAGCCCCCTCACCTTTCCTGTTTCACTTTTGCCAATGTA[C/T]ATCGGGTTTGGTTTTCTTGTATATTTAAACGGTTGTGGTTTCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCGAGGAGAGTTTTACC
WI-18882	94	C	T	---	GTGTGTCCAAAAATGGGGTCTGCTCCTGCTACCTTGACCCTTCCCTTCCTTCGCTTCTCTCCTCATCATCATTCCCAACAACATCCTCTGCCA[C/T]ACACAACAAAACGTAAGTTTCATTGGGCAAAAATTGAGC
WI-19970b	167	G	A	---	TATAAGCCCGAGTCACCAGGACGGCCCTGTCTGGCCACAGACAGGGCTGCTGGAGCCTGCCCACCGGCCCCCGGCCAGTGCAGTCCAGCGGGGAGGAGCCTCCTCACTGCCGGGGACCAGCAAAGGCCTTCACTGGGTTGGTCAAAG[G/A]TAGTCACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACCAGAAATCTTTAAAGACTGACCTTCCTTAAAAACAGA
WI-19970a	126	T	C	---	TATAAGCCCGAGTCACCAGGACGGCCCTGTCTGGCCACAGACAGGGCTGCTGGAGCCTGCCCACCGGCCCCCGGCCAGTGCAGTCCAGCGGGGAGGAGCCTGCCAAGGTAGTCACCTTGGCCTGGTGCATCCACAGAGGATACCAGCAAAGGCCTTCACTGGGTTGGTCAAAG[T/C]GCCTGGTGCATCCACAGAGGATGTTGTTCAAACCAGAAATCTTTAAAGACTGACCTTCCTTAAAAACAGA

ID	Pos				Sequence
WI-19067d	202	T	G	---	TATTGCTGCTTGTCACTGCCTGACATTCACGGCAᵃGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCCGCCATCCCACAGATGGATCTTCAGTGGGTTCTCTTGGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAAA[T/G]ACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067c	153	G	C	---	TATTGCTGCTTGTCACTGCCTGACATTCACGGCGCAGAGGCAAGGCTGCTGCGAGCCTCCCCTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCCGCCATCCCACAGATGGATCTTCAGTGGGTTCTCTTGGGGCTCTAGGTCCTG[G/C]AGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067b	151	T	C	---	TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCCGCCATCCCACAGATGGATCTTCAGTGGGTTCTCTTGGGGCTCTAGGTCCT[T/C]GGAGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067a	57	C	G	---	TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCC[C/G]CTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCCGCCATCCCACAGATGATGGATCTTCAGTGGGTTCTCTTGGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19106	247	T	C	---	TTAATCCCAGCCCTACCCTTGTTAGTTATTTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTCAATTTATGGGGTATAGTAGTGGCCAAATAGCACATCCTCCAACGTTAAAAGACAGTGGATCATGAAAAGTGCTGTTTTGTCCTTTGAGAAAGAAATAATTGTTTGAGCGCAGAGTAAAATAAGGCTCCTTCATGTGGCGTATTGGGCCATAGCCTATAATTGGTTAGAACCTCTATTTTAA[T/C]TGG
WI-18944	147	A	G	---	CAAGGCAAAAATATCAGGAGCTTTTTACACACCTACTAAAAAAGTTATTATGTAGCTGAAACAAAAATGCCAGAAGGATAATATTGATTCCTCACATCTTAACTAGTATTTACCTAGCATTTCAAAACCCAAATGGCTAGAAC[A/G]TGTTTAATTAAATTCACAATATAAAGTTCTACAGTTAATTATGTGCATATTAAAACAATGGCCTGGTTCAATTTCTTTCTTCCTTAATAAATTAAGTTTT
WI-18952	232	G	A	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTAAGTGAAGGATTGGAAGGATTGTTCATAATACATAAAGTTCTCTGTAATTACAACTAAATTATTATGCCCTCTTCTCCACAGTCAAAAGGAACTGGGTGGTTTGGTTTTGTTGCTTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTTAAAATAAAACTTTGGGAAAAGGTGTAA[G/A]ACAGTAGCCCATCACAT
WI-18932d	177	C	T	---	CACACCTCATGCTAGCCTCACGAAACTGGAATAAGCCTTGAAGAAATTGTCCTTGAAGCTTGTATCTGATATCAGCACTGGATTGTGAGAACTTGTTGCTGATTTGACCTTGTATTCAAGTTCAA[C/T]CTTAGTACGTGTGGCTGGTCACTTCGTGGCTGGAGGTAAGAACGTGCTTGTGGAAGACAAGTCTGTGGCTTG

WI-19042	193	A	C	---

TTTGTCAGTGTTGCCTCTCGCAATGCCTCGCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATG
GATAAGGGAATAATAGGCACAGAGAGGTGAACTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG
ACACAAATTTATACTGCGACAGAACTTCAGCATTGCAGTGTAGTAAATAACTCTAACCA[A/C]GGGCTG
TGTTTAGATTGTATTAACTATCTCTTTGGACTTCTGAAGAGACCACTCAAT

WI-18984	208	A	C	---

ATTGGCCCTGTACAGTTGCTTATTTATAAATTCATTAAAAAACACTACAGGTGTTGAATGGTTAAAA
TGTAGGCCTCCAGTTCATTTCAGTTATTTCTGAGTGTGCAGACAGTTCGCACTGTATTAAAT
GTAACTTATTTAATGAAATCAGAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATT
TATCTTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT

WI-18851	90	T	A	---

GCTTCAATTGGCGATTGATTCAGTGCCCACAATGTAAACAGGGGTTGGTAGTTGTTACTCATTTGAAT
ATACCTTTTCCTTATTGTATTC[T/A]GTAATATAGGGATCCTGGAAATGAGACCTGGTGAA

WI-18821b	76	T	C	---

TCAACTGCAGTGTTGCTTCCTCCCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC
ACAGAGGC[T/C]GGGGGTAGCCATTGTGCAGTCATGGCCCGGGGGAAACTTGCCAACCTTCGTGTCAG
GTGCTGTGT

WI-18821a	69	C	T	---

TCAACTGCAGTGTTGCTTCCTCCCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC
A[C/T]AGAGGCTGGGGGTAGCCATTGTGCAGTCATGGCCCGGGGGAAACTTGCCAACCTTCGTGTCAG
GTGCTGTGT

WI-19021a	20	C	G	---

ACTCCTCTGCTGCTGTCCATC[C/G]ACTGTCCTTTTGAACCAGGAAAAGTCACAGAGTTAAAGAGAA
GCAAATTAAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTTCCATCACGTTG
CTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGACGTGGCATCCTACTTACGTGGCATAAC
ACATCTGTGAGCCCATGTATGCTGGGGTTAGAGCAAGTAGCCCTCCCTGTC

WI-18908	70	G	C	---

TGGAAATTCCCTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGGTCAGTA
TGG[G/C][T/T]AGGGAAAACATTCCATCCATCCTTGAGTCAAAAATCTCAATTCTCCCTATCTTTGCCACCC
TCATGCTGTGTGACT

WI-19037b	155	A	G	---

CACGGTTCTCTGCATCGTTACCAGAGCGGCCCTTCTCGGTCTGTATGACCGCGCCAAATA
TCCCCAAAGCTTTGGGTCCTCAAGTCATGCCGGAATTTAGATGCTGGTCATTTTCTGGAGAGGGGTC
CCCTCCCCCTTACGAACACA[A/G]AAACCCAGCCCACATGACTACACGCTGAGCTCTGCAGGGACCA
GTGCCAGGCACTGGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG

WI-19037a	47	C	A	---

CACGGTTCTCTGCATCGTTACCAGAGCGGCCTTCTCGGTCTGGCTAGCCACG[C/A]CCTGTATGACCGCGCAA
ATATCCCCAAAGCTTTGGGTCCTCAAGTCATCGCCGGAATTTAGATCGTGGTCATTTCTGGAGAGGG
GTCCCCTCCCCCTTACGAACACAAAAACCCAGCCCACATGACTACACGCTGAGCTCTGCAGGGACCA
GTGCCAGGCACTGGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG

WI-19064	66	T	C	---

TTGAGGAGGTGGGGTGAACTGCTCCTTGGCAGGGATTTGTGACACTGCATTGCTGGGGCTGTGTTCC[T/
C]CGGGCTTCTCTGGACCTTGCACCGTGCGATACCAGCCCATGTGCCATGTGTATTTGGGTGGGGGGG
TGGGTGAAATAAAGC

Name	Pos			Sequence
WI-18972a	112	A	G	AGGCCTGTGGCTTATGTCACCCAACAGAGAGGGTCCTGAGAAGTCTGGCTGCTGCCTGGATGCCCCCTGCCCCCTCCTGGAAGGCTCTGCAGAGATGACTGGCTGGGGAAGCAGA[G/G]TGCTTGCTGGCCATGGAGCCTCATTGCAAGTTGTTCTTGCCTGAGCACAGAGAGCAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184	C	A	GTTTGCAAACCAACATGTGCTCTTTCAGTCATTCACTGTTTAATATGACATGGTAGAGAAGATAAGGTTTATGGCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTCCTGAAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCATCTCAA[C/A]CTCAACACTATTGACTTTTGGGGCTGGATAGTTCTCTGTTGTGTGGGGGTTTGTCTTGTGCACTGTAG
WI-19016a	161	C	T	GTTTGCAAACCAACATGTGCTCTTTTCAGTCTCTTTAATATGACATGGTAGAGAAGATAAGGTTTATGGCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTCCTGAAAAACCTTAGATACATAGCCGA[C/T]GTATACAGAGGTTCATCTCAACCTCAACACTATTGACTTTTGGGGCTGGATAGTTCTCTGTTGTGTGGGGGTTTGTCTTGTGCACTGTAG
WI-20096	21	T	C	GGTTTTTGGGGGCATTTATTTC[T/C]GATAGAGACTGGCACAAGCTTGGGCTAAGGACCACCCGCCCCCACCCTCATCTAGAAACAATCTCTCTCGCCAGACTTG
WI-19591b	156	C	A	TGGGGCAATTTTAACAAACCAGGCAAAATATCACATATACCTGAATATAAGGTAACTCCAAGCCATGAGTATAAGATTAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGTCCTTAGGGTGGGGAGCTCTTCCCC[C/A]ACTACCCACTCCCAAGGCATCATTTGGGAGAAAAAGTGTCTTCTATCTGGCTAGCTGTGTTATCTCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45	T	A	TGGGGCAATTTTAACAAACCAGGCAAAATATCACATATACCTGAA[T/A]ATAAGGTAACTCCAAGCCATGAGTATAAGATTAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGTCCTTAGGGTGGGGAGCTCTTCCCCCTACCACTCCCAAGGCATCATTTGGGAGAAAAAGTGTCTTCTATCTGGCTAGCTGTGTTATCTCTAGGGATTGCACCTTCTTACACGG
WI-20310	125	G	A	TCCTCCAGCTCGTCATCCTTGTCTTGTGTTCTTGAGGGTTCTCACGGCGCCCTCCAGGCCATGGTTTCTTCATTTAGGTAGGAACAAAAGGCCAAAAGAACATACAAGCCCAGCTCTCTAGAGGCTCCA[G/A]TCAGAACTGGACCCCTTAACTACAAAGGAATCTTGGATGAATATTTTAGCGGGGCTTCAGGAGCAGGTAGCAGAGCCAAAGTGCACACTCAGGCCATCTTCCTCCCAATGTCCTCCCGGGGGG
WI-20860	224	G	A	CTCTCCCCTTAAGGGAGCCTTGGCCTTGCCAGCCCCATTCAGCAGGGATGGAAGTCACAAGACAATGAGTGGAGCCTCATGCCCCTCCCATGGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCCTGTGTCTCCTCCCCAGTGCTGTCGTCACACTTGGGCAAGCAGAGGTGGTGGCAGACCCCAGCCCAGCCTTGAGAGCTCTTGTAGACCGGAAGGAAGGGGCGGTCATT[G/A]GGTGATGGCTTCTGTGGCTCTCTGGCTT
WI-19359a	39	T	C	GACGTGGACAAAGGAGGAGGTTTAAATGAATGAATACTTTGTT[T/C]CATGTTCAAAAAAGAGTATTAATATTTTGTGACTGACTCGTGATGGTTTAATTAATAAGGCTATTTGTCCACCACTCTTCGGGCAATATTCCTGCGCAATATTCCTGGGCCTCAAGTGGGAGGCCACGTGGGAACAAGGCCCTCAGAAAACAAAGGACACAGCCTCCCTGAGCCAGTTCCT

WI-19766b	93	A	G	TGGCCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGCAGGGCAGG AGATGAACCATAGGAGCCAAAAGTC[A/G]GACAAACAGAGAAGGCACACCAAGCCTGAAACCCTC CGGACAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTCCTACCACCAAGCTCTCCGGCCAGTCATGGACTTAT
WI-19766a	31	G	A	TGGCCCTCAATGACTGGTACATTGGAGAAGCT[G/A]TGCAGCAGCATCCTTTTCTGTGGTGGGCAGGGC AGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAGAAGGCACACCAAGCCTGAAACCCTC CGGACAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTCCTACCACCAAGCTCTCCGGCCAGTCATGGACTTAT
WI-20512d	126	C	G	CTTCCTCTGTTGGCTTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAGAAGGGACTTTCCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCCTTGACTGA[C/G]AAAGC TTAGAAAGGAACTGAAATTGCTTCTTGAATATGGATTTTAGGGCGGGCGGTGGGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGGTGGGATCACCTGA
WI-20512c	59	T	G	CTTCCTCTGTTGGCTTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAGAAGGGACT[T/G]TCCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCCTTGACTGACAAAGC TTAGAAAGGAACTGAAATTGCTTCTTGAATATGGATTTTAGGGCGGGCGGTGGGGTGGGATCACCTGA TATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGGTGGGATCACCTGA
WI-19599	230	C	G	GGGCTTAAAATTCCCCTCTGTTGGGACTGGTCTCTCCAGTTACAGCAAAGGATCGCACCCTTTCC ATAACCCCTTCTACATTGGAAAGAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGTAATCAAAACAAACCTCTTTTTCA GAACAGAGAGCGTTAAAAGTAAAAGTAAAGGGCA[C/G]TTCCAAGAGTAACACTGCTA
WI-20679	82	T	C	TGTTTGAAATAAAAATTTCCATGGTCTTAATTGAACTGTATGTTACTTTCTTTAGAATATCCTTTT TTCATTAAAATAATT[T/C]TCTAAACCACTCTATGTGTTCAACCTTCTGTTAACACTAAGATATGGGT TTTTGGAAAGGCCACAAGTCACCAGCTCCATGAAGTGGGCGAATTGGTCCTTGTTTTGGAAAGCTCTC CAGGGTGTTTCTCCAGAAA
WI-19909a	29	T	C	CCAGAAAATAAAGCCTGAATATTCTCTTTC[T/C]TTAAAAATATAATTTTTCCTTCTTTGCTCTTCCAA GTAAATCTTAAAATGAACCTGTCTATTTTAATCTAGGCAATTATAACACTACCTAGGCGGGGG TTTTTCTTTATACCTTGTTCTGTTCTGTACTGTGGAATCAACTAA
WI-20341	221	G	C	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGCTTAGGGGCATGAGAGACATTAGGAAG GCCACACAATTATGAGTAATGAAATGTGGAGGCTGATGAAGCTACTGCTCCCATTGTTTAGCAGGA GGCAGGAAAAGTGATCTGGGGTGTCCTCCGCAGCAAAGGCGTTGGTGTAAATATTTGGGTGACGTCATGC ATCCCCCATGCCATTGGTTTTTG[G/C]ATGTCTCCAGTGAGCTGTTGGGCAAGTCT

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WI-20113	60	T	C	...	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAAGACCTGAAATACTG[T/C]GGAAACAGTAAAAGCAAATTACCACACAATTAGGAGGAATTATTTCAGACATAGGATATTTAAAACATCACTCAAAATACTGGAGCATGATTCAGCAATAAAATTCTATTCCATAAACCAGGTAGATAAATGTCACAGCTTTAAAATATAGTTAAGTACAGTTGATCCTGTTATTCATGGATTCCGTATT
WI-20895	107	G	C	...	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAAACAAGAGCAGCGCAGTGCAGCGGTGTGGCCACTTCCCCACCAGGCAGAACACTTGACTTCATTAAGGCAAA[G/C]CTTTACTCTGTTACTTTTCCTCCCACATAGTTTAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAATATAACTGGTACTATAGGCAAACAGATGCA
WI-20721	72	T	C	...	CCTGCAATCACAAAAGTGGAACTAGTTGATATTTGAAATCATACTTGATTTAACCACCTTCAGAAATTCTA[T/C]AAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161	A	G	...	CTGGATTTAATATTTCTGGCCTAATAACCAAATGTAATCAATAAAAATTGGTCAATATCTCCACCTCATTTCTGCTAACATGTTTGCAAGATTCCCTAAGGTATTGACGACTGAGCAGTCCGGCAAAGTCATGAGACCCTTAGCTGATCTCAT[A/G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAAGCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTTACACTTCCTG
WI-19348c	103	C	T	...	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGGTAGCAAGTACGATGGGCCATGCACTTCTGGCGGGTCGATGAAGAGACTGTTGGTCATGGCGGGTGA[C/T]GTCCTTCTCCAGGCTCATATGGATGTCCTCGAGGTTGCACAGGGAACTGCTCTCGCTTGTGAGAAGCTTCTCC
WI-19348b	98	G	A	...	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGGTAGCAAGTACGATGGGCCATGCACTTCTGGCGGGTCGATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGTCCTTCTCCAGGCTCATATGGATGTCCTCGAGGTTGCACAGGGAACTGCTCTCGCTTGTGAGAAGCTTCTCC
WI-19635	98	A	T	...	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAGCTCTTCTTGTAGGCCATTGTAACACAATGTTAAAAGGTACAGTAAAAATACAGTATTATT[A/T]ATCTTATTGTGTAGCACGGCTGTGAGGCTCATTGTTGAATGAAGCATCCTTAGGCACGTGACTGCATGCAGCAGATATGTGCTGCAGAAGAACTTTGCCTTT
WI-19641a	46	A	G	...	TCCAATTTTCAGAAAACATGTTCCATGTTTATTGTGATAAGCACTAG[A/G]TATTATAGTCTCATGTTTTTAATTTATGAATAACGTCTGATTCATTTGATTTGTATTTGTATTTACAGAAGAGATGTCAGGGCTATCTCATTCAGTTATTTAATAAATATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAAATTTTAAAAAATACTCAGAATGAGGTAGTATTTAATTTTTAATTCATCCACCCTTG
WI-19642b	52	C	A	...	ATATAGAGTACCATCCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCCT[C/A]GGGGTAAACCAGGACTATTGCATGAGCATTCTTTAATACGTATTTGATGGACACAAGTTTCATGTCTATTA
WI-19673b	180	C	T	...	TCTGCCATGATCATCACATTGTGATGAAGAAACATGATGGTCACTAGTAGGTAACTTTCTGTGTCATTGCCTTACTCTCAGTGGAGGTGCTAGTGGATTTACCTACCACCCTGCTTTTGCATCACCACTGTAAATCTAATAGTGAAAAGGCAAATGATGTCTCAGTATCGTCAGTATCATCACTGTGAAAACATTTTC[C/T]CTTGGACCAGCTGAAAGAAGCCTTGAGGAGCCTGAAGGCTTCAAGGTCCCACACGTCCACAGATGCAAAAAAACACAGCCC

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WI-19673a	35	G	A	...	TCTGCCATGATCACCATTGTGATGAAGAACATGATG[G/A]TCACTACTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTGCATCACCACTGTAAATCTAAT AGTGAAAAGGCAAATGATGTGTCTCAGTATCACTGTGAAAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGTCAAGGCTCCACGTCAAAAAACACAGCCC
WI-19724	35	A	G	...	TTTATTTGGGAAACAAAGGATTGTAATTTGGGTAA[A/G]CTGAGTCACGGTGCCCTGAGTAGTGTC CTAGAAAGCAAACACGAGAGTTTTGGTTTTTCTCTT
WI-19307	196	T	C	...	TCCTCCTCCCCAACTAGATGGTATTGATCACTCTGCCCACAAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTTGCCTTCATGAGAAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGCTGT GGTGAACTGCAAAGAAGGAAACCAGGCAATGTATTCCATAGAGGCCTTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGTGTTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85	A	T	...	CTTTCCCTCATCCCCTCTTCCACCACCACCATCCGGAACAAGTGCTCCAGGATTCCCTGCCCACTGGC CATTTTGGAGTGTGTCC[A/T]TGGGTAGCAATGTGGAAACCACCAGGGCCTTTGTGGAGAAAATGG AGGGGGTTGAGGGAGTCCCAGGAGGGGCCTTATTTGCCCACTTGCTCATAGGCCGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCGAATTCTTCCCGGGCGTAGGCA
WI-19946	122	C	T	...	CAATGGACTGAATGAGTGCGTGCTGGGTGGGGCACACACCTTCAATACACGTCAAGGTCG CTTCCAGTTTAGAAAAACAGAAATCTGCATCTGCAGCCTGAGACGCACAGAGAGGT[C/T]TCTTCCTG ACCCAGACGCACTCACGAGCGCAGGTCCTGGTTTCAAAAATGCATTTAACCTGCGCGCAGAGAGTTCAC CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G	A	...	CACAGCCATGGTGTAAAATAGCATCAGATTGAAATGAAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACTTTACAGCACACATTTTTAGGGCCAAGGTTTGGATCTGTCTGGACCT CAATGTT[G/A]CTCTCGGAGAAGCAGCCACGTTAGCACGAGATACCTTACAGCTTGTCATCTACTCAA GTGATGGCCAACAGAAGCTTCTGAACTCCTCCTGGGGGAGGTAGCTGACAAG
WI-19076	40	G	A	...	TTGGTTGGATACTTGCTGCTGGAAAAAAAAGCAGTTTTAAT[G/A]TATTCAAAAATACCTTTTAAAAA GTATTCTAGCACAAGATTTTTCTGTAAACTAGATTATGTTGTAAATCTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTCCAAATCTATCTTGCGCTCCTGAAAAACTGCAGA AAGGCACTGAAAGCTGTTTCTTTAAGATATGGGATTTCTTTTATTCTT
WI-20218	26	T	C	...	CCACACACTCTGGTTTTATAAAGCTA[T/C]AGGACAGAGCAGAGATGGAACTGAAAAAACAGGGTAG AAAATAACATAAAAATTGGAGGGGAACAGTGGGATGCGAGAAAGAAAATGACACAGCCACATGTGCCCCA GTCAAAATACTTTTAGTCCCTGCGAGCAAAGATGCCAACCAAGTCTCTATACTGGCTGGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T	G	...	CAACCTTTTTGACAAGGGGACGGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAATATCTCCAGGCTTGATTGGGAGGGGCTGGCCTCTACCCCTTCTTCTTTCCA TCCAGTCTATTGCCAGAT[T/G]CCAGAGAAAAGCGCGGGAAAGCCCAGCTCTCCAGCATAGCCACTGTGG GTCGGGCTTCACCTTCTGTCGACTCCTCATGCTGGGACTTCGTGTCTTTCGGGG

WI-20361a	192	G	A	---	CTGGGAGTGCTGACCTAAGTGACATTTTTTTTAATGCCAAATACAGTAATCTCCAAGCTTTTAATGG CTTATGCAAGATGACAGAGAATATGTGAAATCTGATTGTCCCAGAGTTACACTCTGCACTCCAAAGCTA CAACAGTGCCACAGCTGCCACAGTTCCTATACTTCCTACTACTGGTGCACAATTTAGC[G/A]ATCCTTC AAATGGGAAAATTCCTAACTACACGAGACAATGGGTCCTACAGTAGGCCCG
WI-20572	75	A	G	---	GAGCCAAACCCAAAACAAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTTCTTCT TCAGAATT[A/G]TCATAAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCA AATTTCATCTTCTCTCAAATTTAAAATTGTTTAATCCCAAAGGTGCCTATTGAATTCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G	A	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAGAAAAATGTGAGATCCTTTGTTGGTTTTTTATTTCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTTCCGCATTCAGG
WI-20593	79	A	G	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACAAACTCCAGTCTTTTCAGTCTGTTG CTGTACTTCAG[A/G]TTTAAAATCTGGGAATGAGCATGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAAGGAACTCAGGATGTTGTTAGGAGAGGGGGAGTGGATGCCAGGCCTTCACCAGACTAT CCAGAAGCCATTCCATGGGGTATTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57	T	C	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCCTCA[T/C]ATGTATCT TGTCCCTGCTGCTTTTAGGTTAGCAAGGTGTATGAATACTTTAAGTTTGTTTGTTTCTTTCCTCGT GGTATCAGTGAAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAAATTGCCATGGAACTGAGC AAAAGGCCCACGTGGGGATAAAAATCACTCACCATCGACGCCACCAGTATT
WI-19066i	239	A	G	---	TGACAAGGGAGAGAAGGGAGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTAAAACCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCTGTGAATTACTTCTCCATATTCC[C/T]GGATGCTGCTCAATTACAGT ACCATTGCAGGCCAAACTTTTTTTCTTAAACGCCCTCACT[A/G]TTTCTTTTTA
WI-19066g	184	C	T	---	TGACAAGGGAGAGAAGGGAGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTAAAACCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCTGTGAATTACTTCTCCATATTC[C/T]GGATGCTGCTCAATTAC AGTACCATTGCAGGCCAAACTTTTTTTCTTAAACGCCCTCACTAGTTTCTTTTTA
WI-19066f	148	T	C	---	TGACAAGGGAGAGAAGGGAGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTAAAACCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCG[T/C]TGGTCACCCTGTGAATTACTTCTCCATATTCCGGATGCTGCTCAATTAC AGTACCATTGCAGGCCAAACTTTTTTTCTTAAACGCCCTCACTAGTTTCTTTTTA

			Sequence
WI-19066e	147	G C	⫶	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAACCTTCAGCTGATC[G/C]TTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC CATATGTTCTTGCG[G/C]TTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTTAGTTTCTTTTA
WI-19066c	100	G A	⫶	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAACCTTCAGCTGATC[G/A]TCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTTAGTTTCTTTTA
WI-19066b	87	C T	⫶	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAA[C/T]CTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTTAGTTTCTTTTA
WI-19066a	72	C T	⫶	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTTAGTTTCTTTTA
WI-20660	105	G C	⫶	TTTACAGCGAGTTTTTCCGTCTCAATAAGTAATCTAAATAGATTAGGGTGAAAAGAAAATGTG TGTCTAAATAAAATCTCCCTTTTGAATGTATATTTGT[G/C]TTAATAAAGGGAAGCATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCATTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCCAAAAAATACTGTTTAACACACTATGTTTTAAGA
WI-18768	120	C T	⫶	CTGCTGCCAGCTTCTCTCTTGGCCCTGCCTGCCCAGATGGCGGTCCTGGCAGCCTCCCCTCAGTCTTCC TCCACCCGCCCCTCTTCCCAGCCTGGT[C/T]TTCGGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37	A G	⫶	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGT[A/G]TATTTAACTTCTAGTTGCTTCTTGCTTTG GTCTTCTTCCAATGATGATGCTTACTACAGAAAGCAAATCAGACACAATTAGAGAGAAGCCTTTTCCATAAA GTGTAATTTTAATGGCTGCAAAACCGGCAAACCTGTAACTGCCCTTTTAAATGGCATGGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-18790	49	A T	⫶	GAAAGCCAGAGAGATTAGCCCGGCATTCCGGACTCGTCAACCAGGACAGAA[A/T]GCATGGACAAGAGGGA TGAGCTTTACAAAGATGATGCACTTGGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCCT
WI-18987	35	G A	⫶	AGGAGGCGTGTTCCAGGAGTCCTGCCCAGCAGCCTC[G/A]GTGGCCAAGCCCAGACACTCACCCACCTT CCCAGTGGCCCCGTGGCCCGTGGATCCTGGATCCTGGTCCTAGGCTGGACACAGGATTCAGAAAGACACCAGCGGCTGCACA GAAAGAGCAGAGCCAGATGGACCTGAGTGTCGGCCACACTCAAGGCCTCAAGGCGTGAGAGGCCTCAGGAA AGTCA

Marker	Pos				Sequence
WI-18919	26	C	T	---	TGGATGAAAACCACAGGGATTCCGGA[C/T]GCCAGACCCCATTTATACTTCACTTTCTCTACAGTG TTGTTTGTTGTTGGTTTTATTTTTATTTTTATACTTGGCCATACCACAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI-18741c	64	G	A	---	CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGAGCCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G	C	---	CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCA[G/C]ACAGAGTATCTCTGCTCTAGAGCCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T	G	---	CTTTCTGGTCAAGGCTTTGGACA[T/G]CTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G	A	---	TCAGAAGCAGACAGATGGCATCGTGTTCCTTGCTTGTTGGTTGTGTACCTTTCACGAGACCTGAATT TTAGAATTGCCCAGTGCTGCCCAGAGTGAGTGAGTGAGTGAATTCTCCTTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTCATAAACATATCAACCA[G/A]TAGCATTAACCCATTTATTTCCTGTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46	T	A	---	CCAAGTTGCATCCATGTTTGATTTCTGATGAGACTAGAGTGACAG[T/A]GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGGAAAATGCAGCTGC ATAATTAAACACATTATCAAAGTCCTCTACAATTTATTTCCGCAGCATGTCAGCTAAGTGTCACTGCCATAT ATGGGGAGAGAAAATGCCTGCTTTCTTCCCTCTTTTCTGCACTGGTAGC
WI-19183	210	G	C	---	CTGTTGAAGGCTTCCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAAGCACACATTGGATG GCAGCATGGGGTTCTTCCCCATTTATGGGCATGAAATATGTGGTTTAGAATAAAGGAACAAGCATTATT CCTTGCCAACGCCTCACTCTAAGAGAGGCTTTTTGCTGAGTCAAGCAAACACTTGCCTGCTCTGCCC CTTGGGAG[G/C]TGCATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	T	C	---	TTGAAATCCCAGTCTCCTGGCCCCCCAGGCAGGGTCTGTCACCATAGAATGTCTTCCTCTACTGGGGTC GTCTGGCTTTTGTTAGAACTGGTCTGGATGTTCTTCCCCGTCCATTACCATTCGGATGTTCTTT TGTTCAGAGCAATGTTTCTTGTATTCTGAAACTGGAAACTGAACCAGTTTGCCTTTCTCCTAGTCACC AAGCATACT[T/C]T[C/T]CTCCTGGCTCCCCAGTACTTAAATGTTCTCATCTGT
WI-19041	198	T	C	---	GTCTCCCCAGAGTGCTTCTGCCACCCCAGCCCTGTCCTGCTGTAAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGCCCTTAGTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCCAAGCTCATCACACACAGGGGCCCATCCTTCTCAATACAGCGCT[T/C]G CCCTTGCCAGTCCAGTCCCTATTTCAAAATAAAAATTAGTGTGTCCTTGTCCTGTCTGT
WI-19135	20	G	A	---	CAGTTACCCTGCTTTGCCTCTC[G/A]AAAGTGTCATCAATTTGTAATTTGTAAATTAACTCTGTAAAAGT GTCTGTAGGTACGTTTTATATTATATAAGGACAGGACCAAAAATCAACCTATCAAAGCTTCAAAAACT TTGGGAAAGGGTGGGATTAAGTACAAGCACACATTGGCTTACAGTAAATGAACTGAGCTTTATTAACT GCTTTTTGCCCATATAAAATGTGATATTTACTGGGAAAACCTAGCCAGCTTCAC

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WI-19236	54	G	A	TACACAGAGGGTGCGCACTTGGACTCTGAGGGTTGGGTGTGTGGAAGGGGGGAAAAGG[G/A]GATGGGAGAC CTGCTCCCCAGCTCTTCCTGTCGCAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTTAGGGGAGGT CACCTTACCCTTTTCAAGGGCAAAGAACTCGTGGGAGGATGTCTGTTGTATGTAATACT AATCTTTCAAGGGCAAAGAACTCGTGGGAGGATGTCTGTTGTATGTAATACT
WI-19144	222	G	C	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTCATTCAGCTTGCTGACCTCCCAGCCTTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCACCAGGAGGACTGGTTGTGAGCTATCTATATTCATTCATAGCCAA ACAGGAGACCCCTTTGCACAGACTTGCACACAGGGAGGCGTGACCAGGAAACCCTCTTCTTCCCTGGT CTGGCTCTGCTGGAGCGGG[G/C]TGGGAACCAAACACCTTCAGTGCTGGTG
WI-19139b	110	C	A	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGGTTGGCAGACAACACACTAG[C/A]ATTTTCACGGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTGCTCTCTTTGG GGGGCCCCGGAGATCTAGCATCTCTGAAATCCTGGCTGTCGTGTGAGGCTTTGAAG
WI-19139a	66	C	T	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAGACTGAACAACGTGTATTTACACGAGGGTAGA[C/T]GGCAGATGCCTGACAGAGAGTGGGTTGGCAGACAACACACTAGCATTTTCACGGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTGCTCTCTTTGG GGGGCCCCGGAGATCTAGCATCTCTGAAATCCTGGCTGTCGTGTGAGGCTTTGAAG
WI-18910	112	T	C	GGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAGAACCTAAACATGAAAGGAAAGGGTGCCT CATCCCAGCAACCGTGTCCTTGTGGGTGATGATCCAGTCACTGTGCTGCTTGT[T/C]CGGCTCATGGCAGAGCATT CAGTGCCACGGTTAGG
WI-19235	173	A	G	TTCAGGAGGTGGAGTTCGTCGTCGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAAACA CGAATGTCTCTGTAGCTTCCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCCTCTGT CACTCATGCCTTGCCTAATTGTTCACAATGGTGGAA[A/G]GCTTCATGTAATATGATCAGGAACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCGAGCACTA
WI-19222	179	C	T	CGTTTCCCTAACTCACCCAGTTAGTTTGGGATGATTGATTTCTGTTGTTGTTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTTCTGTTAGGTGAGTGTGTGGGTTTTTCCCCCCACCAGGAAGT GGCAGCATCCCTCCTCCTTCCCCTAAAGGACTCTGCGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGGTACACTGACGTGTCCAGAAGCAGCACTT
WI-19117	134	A	G	AAATAATGCAACGCAGGAGGAGAAAAAGAGAAAATGCACTAAGACAAGAACATTCTCTCATAGAACATTG ATCTGTTTTACAGGAAACAAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTTCCTAAGACATTTTCATTCATGAATATTTTCAAGTTTTTCATACTGTACA CATTTCTTAAAACACATGATACCAGCAACTGAAATGAATGCCGAATTTG

ID	Pos			Sequence
WI-19134c	263	C	T	CTCCTGTTCGTGACCTGACACAGGGTGACACAGCGCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAAGTGGTCTTCCATCCCAGCAAGGGGTGCAGCCCAGGGTCAG GCCCTTCAGAGCCAGGGCAGGATGCACGGTGGCTAGCACCCTGGGTGGGGAAAGGG TTCATCCACTTGCCTCCTCCCCTCTACCCTGGCACCCTGGGTGGGGAAAGGG
WI-19134a	162	T	C	CTCCTGTTCGTGACCTGACACAGGGTGACACAGCGCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAAGTGGTCTTCCATCCCCAGCAAGGGGGTGCAGCCCAGGGTCAG GCCCTTCAGAGCCAGGGCTAGAGGA[T/C]GCACGGTGGCTAGAGCCCAGCTGCCACTATCCTTTTCAGAG CACTTCATCCACTTGCCTCCTCCCCTCTACCCTGGCACCCTGGGTGGGAA
WI-19224	112	C	T	GGTTTCACCAGTCTTCCCAGGGAACTCCGATGAAGTGTTCCAACAAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCT[C/T]CAGGATGCCTGTGAAGA AAGATCCCTGGATCCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCAGGCCAGAAGACTTCC AGGGAAACTCATTCAAGGAGGTGAAAATGATGACTCCTCCAAGATGAAAA
WI-19201	179	T	C	GCAGCTCCTAAGGACCACTGGCCATTAGCTCTTGCTTTTGATGGCATTCTCTTTCCACCTTGTCTTCTC CTTTGCTCTCTGTGTTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCCGCCCCCCACACTTTGCCTGCAGGTGCACCGAAAGGAC[T/C]TGGGGGATAAAATTCAAAAAA GTGTGATGTGCTGCTCAGAAGGTCAGACTCCATGTGTCTGCCTTGGCCTCAA
WI-19034	45	T	C	GAAATGGCTCCACTCAGAGCTCACCCCGGTGATGAGGATAGGGGAA[T/C]ACTTCTCTATTACATTAAAG GCAACAGCAGTTAGTAGTAAAAAGGTTTTTCACAGTGTTTCTGCTGTTTGAAAGTGCAATATAAATTTTTG CTAGCCCATGCATGATCAATCGACTTCTATTGTTTGATATACACTTCAGCATTTAAGTTCTGTCGAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGTCTATATA
WI-19102	25	C	G	TGTTCCTGAGTCACGCTGAGGAGAG[C/G]CTTCACTCAGGAGTTCATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCCTTGGAAACAGAATGAAGCAGAGGAAACTCTTAATACTTAAAATCGTTCT TGATTAGTATCGTGAGTTTGAAAGTTTTGAACTCAGTTTTTGAACTCAAGGGAGAAGGTAT AGTGGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A	G	AAAGGAGGGAGAATCTTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCCTCACTGGGGGAA[A/ G]AAAAAGCATCT[N]TCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G	A	AAAGGAGGGAGAATCTTTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCCTCACTGGGG[G/A]A AAAAAAGCATCT[N]TCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T	C	GGCAGCAGCTTTTTAATTGAACACTTTCTTCTTGGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGGACGGCAGAGC[T/C]AAGATCCACAATTGCAAAGGCCCACTGCTGGCTCA CTTCCTCACA
WI-18501	121	C	T	CAGAGGGAAAAGTTTATTGAGTCAGCCACACAGAGGAACAGAGAAACAGAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGGNACAGCTGAACCCTGCGCCAGGACAGCTGAACCCTGCGCCAGGAGGGCG[C/T]GGACAGCA GCGCATGCCACAAACATTCA

Marker	Pos				Sequence
WI-18017	87	C	A	---	ACAAAAGAGAAAATGGAAATAGGTTTGCGAAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCATTAAAATTATATCTCTTGCAT CAGAGCTGGTGGAAAATCAT
WI-18148b	101	A	G	---	TTATTGCGTTCCTTCGATAACCTCTCTTGGGACTATGAGATCATCCACCAGATGTGAAAACGAAAGCA GTGATTTCAGAAACCNTCGATTCTGAATATCCC[A/G]TGGGGCATATGCAAAGGAAGATGA
WI-18254	64	T	C	---	TATACGGATCATGTATTGTGTGACCACCACCACCAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]GCCAAAAATTCCCTCTGCTTCCTTGTAGTCAGTCCTTCTCCCAACCCCAGGNACTTGGCAACCTGTTT TCCGTTCCCTAGACATTT
WI-18265b	117	C	A	---	CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAGACGGCCTTCTGCGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTCGTGCTCTAAGTGAGCCATGAACTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGTGGTTTCTTCAG
WI-18295	40	C	T	---	ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATTCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64	T	C	---	GGGCAAGAGAGCAGAGAGATTTAATTGAATAAAAAACTCCAGGCTGTGACACGGGTGGGAGACAAAA[T/ C]GAGTAATTAACACACATAATATTTANATGACAGTGCAATTAATTAACGTCCTGGGTAAGCCAGAG GGGGAGGAGGGGGTCTTTCA
WI-22585	56	A	G	---	TTTATTTAAATTTGCATCCTGAGATAATAAAAATTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAAGTTTCGGAGAGGCAGGTATCCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A	G	---	GGGCTGTGGAGTAACAGAACTTGATGGAAAATTGGC[A/G]TCTGTGTAGAATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G	A	---	GCCTTTGCTCTTTGCTGTCCTCAGAGGCCTCAGATGGATACGCAGCAACTTCCTTTGAACCTTTTTAT TTTCCTGCAGGAAGAAGAGA[G/A]GGATCCAGCAGTGAGATCAGCAGGTTCTGTGTTGCACAGACAG GGAAACAGGC
WI-19888a	98	C	T	---	GGCACGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCATTTAAAATGGTAATTTCATGTGTATTTATGTGANCATATTTATGTTGGAAGTGAACACATGT CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C	T	---	TGAGACCATCCTCCTCAACAAAGAATCAGTTCAGCACCTAATTTTCCCACACTGAAGTCTACG CAATTTTCATGCAGA[C/T]TGTGCACACAGTGCACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T	C	---	TCAGAATTGCTTTCCCACTGCCCCAAACCAAAGAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTAAAGAAAGGTACCTTCCTTGGAGGTTGCATGACAGGATTAGTCTTCTCTGTTT[T/C]CTTGGT GCAAGTTGAACCAGTGATTATGTACCATTGCATCAGAGCATCTGTTCCCGTCAGATCCCAACTAG

Name	Position			Sequence
WI-20561b	94	T	C	CGTTGCTTATTTAAGATGGCTGTGTTATAAGTATAAAGCAGTTGGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACACATG[T/C]GGAATCAATGTCTTTAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25	A	G	CGTTGCTTATTTAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTGAGCAACACTGATTGTGCATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69	T	A	GCTTTCATTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A[T/A]ATAAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCACTTAAAAATGNCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGCCATCAGTCTGCAATTCCCGAGATAA
WI-20116c	59	T	A	GCTTTCATTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGT[T/A]TAGAA CATATATAAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCACTTAAAAATGNCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGCCATCAGTCTGCAATTCCCGAGATAA
WI-20116a	22	C	G	GCTTTCATTTCTGTCACCCAC[C/G]CTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCACTTAAAAATGNCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGCCATCAGTCTGCAATTCCCGAGATAA
WI-20466b	133	G	A	AAAGATTGCAGTCCTGGGACACAGTTGGAAAACACTATTTATAAGGTTGCACATATTACAAACAG NTCCCAAATGGTGAAACTGGTATTCTAAGATGAAACTTAATGAACATAATGAAGTGAATAAACGC[G/A]TGTGAACTAAATGTTTAAAAAGTTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTATCCCTTCAGGTCGATT
WI-21444	39	A	G	CTGGGCAGCAAGTAACCATTTAAAGAAATACTCTCAAC[A/G]AGTTCTTTTTTTATGGGTATTTCA GTTGTTAACAAAGTTAAAATACTTATTGGAACTAATCTTTGTATTTATTCGAGGAAGAAGAAATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI-21034b	148	T	C	AGAAATGGACAATGATGCAGATGATTTGTGATGAGGATTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTAATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGA[T/C]GCCTAACCTATCTCAATTTAAGTAATGTGAGCAA
WI-22091c	205	G	A	GGGCGTGTATTTGATGCAAGTCCAACCAGTCAAGCTATCATTGAAATCCAAATATTTCCCAGTAGAG ACATGCAGAGCAATGTCAATGTAACATACAAGCATATTACCTCCCCCTAAGTGACTCATAATTTC ATTACTTGTCTGTCTGTAGCTTTAAAGGTTAAAAAAGTTGTAGCATTAAGTGGTATTTACTGAGGGCA ACA[G/A]AJAATTACGGCCTTAACACACTAAAATCATGAGGGCTCAGGGATTG

ID	Pos			Sequence
WI-21805a	45	A	T	CAACTGCTCTGAGGTCTTCACTAGCTGATTATAATCCTATATT[A/T]AAAAAAATCTATAGTCTG CAGTCTTTGACATACTTCTCAAGGGTGGATATGTGGTGGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGCTTTTTGTAGCTTAACTGCTGTTTAGNAAATCCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGCAGTTGAAGGCTGTTTTTGTTAATTGCTG
WI-21778b	155	T	C	AAAAATCCATAATTATTGAAACCCAAGTTACAGAGAAAGTTCGTAACTTTTTTATTGAATTATTGAC TCTGCCCGCGGTGTCGTTCGTCTGCTTTCAACTCCAGTCTCAATGCCCCTGTGTAGGTGGGGTCCCAG GTCCTGGGGCTTCTGAGGTCC[T/C]GGTAGAAGGAGGGGCAGGTGGT
WI-20907	241	A	C	TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCGCTCCCTGACTCCGGAAACACTGTGCCTCT CAAATGATCTAGAGCTCATCCTTGGGCGTACACTGGGGCAGTTGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTTCAAGCCAATTCACACTGGGAAAAACACACCCTCACAAGATGCCTATCCATTTGAGTTC ATACAGGTTTAGTAGCTAGAACTAAAAAAACATTTTA[A/C]AATTATCTA
WI-21449b	222	C	T	AACAGCAGCAGTCACTTCCAAAATGCAAAAAAAATTACAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACAACAGAATCAAATCACGCAGCACTGGAGGCGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAGCTGACAAGAAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA[C/T]TGACAGAGCCCAGTGTCTCTGGGTTAG
WI-21558a	157	G	A	GCTTACAAGGAAGCCTGTGGACAGGCGAGNTGGGTGGAACCGACTCCAGCCTGGAAAACCTGCCCTC CCATCCCCCTTAGCGCCTTCGCGGCTGATTTTCTTCCGGCTTCTTGGCCAGGGCAAGG AGCTGTGGTGGGGGGCAGTAT[G/A]AGCCAGGACTCCCTTCCCACAGATGAGGGCCTAGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178	G	A	TTTGCTGTGTGGAATCCATGAGAGCCGGAAGCCATCGTTGGGGCCGTGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCCTGACCAATGGGTGATTACATTTAAAAACCAAAACAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG[G/A]AAATTTCATGAAAATTTCC CCTAAACCATAAACAAAAACTGTCCTCCTTACCCCAAAGTGCTGGAGGAAAG
WI-22187a	110	C	A	TTTGCTGTGTGGAATCCATGAGAGCCGTGTTGGGGGCCGTGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTGGAAATTTCATGAAAATTTCC CCTAAACCATAAACAAAAACTGTCCTCCTTACCCCAAAGTGCTGGAGGAAAG
WI-21609b	146	G	A	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAACGTGCAAGCTGTAAA AACAAGCCCAAACCCAAGACATCACAAGAGGCAAGGCAGTGGCAGCAGTGAGAAGGGAGCCTGTAAAG GATGTTTCAAAG[G/A]AGGGTCCCGGCTATGTGGCCACTGAGCAGANTGGCCAAAGAGGAGTTGGAG TTTCGGGTCTGGGAAGTGGCAGAGGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

ID	Pos				Sequence
WI-21609a	42	C	T	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAA[C/T]GTGCAGTCCGTTCACAAGCTGTAAAAACAAGCCCAAACCCAAGACATCACAAGAGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTAAAGGATGTTTCAAAGGAAGTGGCAGAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGCTTTCGGTCTGGGAAGTGGCAGCANTGGCCAAANGAGGAGTTGGAG
WI-22512a	104	T	G	---	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAAATCCCTTGGTGCCTCCTAGGCTTCAGGGTAAGCCCTGACATCATGGTCCTTTGTGATCTGT[T/G]ACCTCACCCATGTCTCCCACCTNAGTTCCCACATTCCCCCACGTCTCAAGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139	A	G	---	ATCGGCAAGCTACAGCCTTAAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAAGGGCTCACAACACTAAAGATTTCACATGAAAGGGTCGTGATTGAGCAATCTAGGGGATATGTGACAGGGGTTTC[A/G]TGCACTGGTACAGAACACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATCTACGG
WI-21028a	121	A	C	---	ATCGGCAAGCTACAGCCTTAAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAAGGGCTCACAACACTAAAGATTTCACATGAAAGGGTCGTGATTGAGCAATCTAGGGG[A/C]TATGTGACAGGGGTTTCATGCACTGGTACAGAACACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATCTACGG
WI-18829d	58	A	G	---	ACAACATGCCTGTTCACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]TTTCATCATACAAGACAAGCACAAAAGCACCACCCCATGCCTCTGAGGAACATTGGACCATGCACCCTTGAAAA
WI-18829b	35	T	A	---	ACAACATGCCTGTTCACAGGGGGAAAAATCCTAGG[T/A]AATAACTTATGTGTACTTCTTGATTCATCATACAAGACAAGCACAAAAGCACCACCCCATGCCTCTGAGGAACATTGGACCATGCACCCTTGAAAA
WI-20964	87	G	A	---	AGCCAACTCAAGGCCAAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGGAGGGGAAGCAAAGGAGCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAATTAAAAGAATACTAAGATTAGATGAACAACACTCAGAAATACTCTAGGGAGAGCTGAAAAGAAGGAAACAGATGTTAACAAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59	T	A	---	CTCTGAACTAAAGGGCCGTGAAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAT[T/A]ACATTGGCTGGAATGAGGTGGTCAGGAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGAGTTCTGGAGAAGTGTAAAGTGTAAATAATTACAAAGACTGACAACTCTTACCTTACATTATTCATCTACAGACTATTTTCTCCCTTAGGAGGATGAGGAGTATGGGCCTTAGGT
WI-22130b	165	C	T	---	TGTTTTTGAGGGGCTGTAGCAGACTACATAATGAGCGGTGAAAGCGGCTGCCTTCCCCTCTCCTGACACCAGCAAGGGGAGGGGAGCCAGCACCATCACCGGCCCGTGCCCCATCCAATGATTACTAGCACTAGGAAGCCAACGGAANAGGACCCCGCGCGCTTGCT[C/T]GTGTTTAATCCAGGTTAAGCTATACACGTTTAAATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

ID	Position	Alleles	Sequence
WI-21661	117	G C	GCTTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTCCAACTTTAGAATGTATAAATAAGAATGACATTTAAAATAAAATA[G/C]TTTAGTCAGTC ACACAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTGTGCTTTCAGCTATGAAG GA
WI-21980a	25	T C	TCAGTTTAAACACATTCATCAAGGA[T/C]AGATTAATTAATGTCAGGTGAGCATAAAAGGGGAGATTA TAAACCAGAAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTCAT GGGTGAAGCCCCTGGGATAAAG
WI-21636	71	A G	TGCTTGTATTAATGTGGTGTTGTTTACATTATCCTATTTCACAGATGGAAACAGAAAATACCAGCTTTTT AAA[A/G]TAGCAATATCTATTATTATAATAAATATTGAAATAACACCATAATAATATCACTAAGGA AGTAATCTAATTGTGTTGATTTGCAGAGGGGAGAAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAAACTAGGAAGGGACAGAGGGATTTC
WI-22457a	112	G A	TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAAACAGTAAACATACTGGACACGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAG GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGGAAACAGTAATGCGAGATTAATACCTGGGGCC AAAACCCACTGAACTCACCCCAGCTGAAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97	C T	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACTTAT AATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCTGCAAATGGACTATTGCC CAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTCCAGGGGATG
WI-21524a	35	A C	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGTACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTCTGCAAATGGACTATTGCC CAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTCCAGGGGATG
WI-22652a	32	G T	TTACCTTCCAAACCAGGCCACTTTGGAGAAAG[G/T]AAGAGAATGCTATTAATCAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCACCATTCCTGCCACAGAACC TTTGCACATGCTGCCCTACTCCGCCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCCATCCCTT CTTTAGGG
WI-21703d	197	A G	CAACAGGCTCATGGAACAGAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGTGGGGCAGGGCTC TGCATCCCCTTTCCTCAGCACAGCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGGGAGTGAGTCTGGGAA[A/G]G TGGGCAGGAGCAGCAGCTAGGGGCAAGGAACTTAAGGGAACTTGTGGGGAAGAG

ID	Pos			Sequence
WI-21703c	134	A	G	CAACAGGCTCATGGAACAGAGACCTAGGAGCATAGGAGGAGTGGTGGTGCTGGGCAGGGCTCTGCATCCCCTTTCCTCAGCACC[A/G]CTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGGAGTGAGTCTGGGAAAGTGGGCAGAGCACAGTAGGGGCACAGTAGGGGCACCATCTTCAGCCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGGAGTGAGTCTGGGAAAGTGGGCACAGTAGGGGCAGAGCACACATTAAGGGAACTTAAGGGAAGAG
WI-22663c	139	G	A	CCCTTGTCAGTCTGTGCCTCGGCCTTCTCACTGCACTGGCGAGGTGAGCCGGCCGCTCGCGTAATCTTATTCCCAGTCTCGGTGAACATGGCCTCAGTCTCTCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTACGC[G/A]GAAGAGCTTCCTCATTGCTGAGGGCTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663b	55	C	T	CCCTTGTCAGTCTGTGCCTCGGCCTTCTCACTGCACTGGCGAGGTGAGCCGGCCGCT[C/T]GCTAATCTTATTCCCAGTCTCGGTGAACATGGCCTCAGTCTCTCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTACAGGCGGAAGAGCTTCCTCATTGCTGAGGGCTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663a	38	C	T	CCCTTGTCAGTCTGTGCCTCGGCCTTCTCACTGCACTGG[C/T]GAGGTGAGCCGGCCGCTCGCTAATCTTATTCCCAGTCTCGGTGAACATGGCCTCAGTCTCTCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTACAGGCGGAAGAGCTTCCTCATTGCTGAGGGCTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22668	99	A	G	TCTTTTATCCTGCTGCCTGCCTGAGTATTCTGGAATCCTACAAGGATTTGAGGAGGAGCCCTTGGGATTCCAACCTAACAAATTAGTTTCTGTAATATT[A/G]TTCTAGTCCATTAGATTGTGTAAATGATCTAAATGGNGTAAACCATTTAATATCAAAAGTATAAACAGCATTAAGTCAGCTTTTGAAGAAACTTTATT
WI-22631a	52	T	C	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTTCAGTTCTGA[T/C]AGCACCATTTTCAAGTTTAGGCAAGGTATTTAACCTCTCCAGGCTCATTTCTCTTTGTAAAAATTGTGATAATGGACCTATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI-20258	157	G	T	AATCCACACTTTCACGGAGGGGGACCAGCCTGCCATGTGTCGTCCCCAGGCTCACAGCAGCGGCGGCTACTCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATTGGAAACCGTAAGGCATGACAACGGGAGGCCCGCGGGGTGTTTCAG[G/T]CGCGTTGACGGCAGGTGCATGCGGCAGGCCCTCTACAGAAGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAAGTACC
WI-22714	212	C	A	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAGAAATCTAGGGTCTACTAAATAATCTAGTACTTGTTTCCACTCTCCTGCTAACTCTGACAGGAGTGTTGTTGGGAAACGAAGTCTGAAAAGGATTCAAAGGGGGCTAGGGGCCAAACATCCTTAACAAGCTAGTTGCTACCAACCCCA[C/A]TGAGTAGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G	A	TGGGGGCTACTTTAGATGGGATGGCCGTCAGGGTCTGGGAAGGCCT[G/A]TCTTAGAAGACATTACCCAAATGATGAGAGGCAGCCAGTCGTCGAAGCCATAGTTTGGATGGCGAGACTTTCCGGCCAGAGGAAATAGCAAGTGCAAAGGCCTGAAAGGCCTGAAAGGTGAAAGGCGGCCGGTNTGGCTGAGGTTTAGTTGGATG

WI-22724	117	A	G	---	TGATATGATGTCTGAGATTTGCTTCCAAATATGCCTAGGAAGGGAAGAAGTGTTTAGAGAGATATAGGACAAATCAAGATTGTCAAAATGTATAGTAACTGTTAGTAACTTGCTAAGGGT[A/G]GTTATTCTATTTTGGGATATGTTTGGGAATT
WI-22750	48	G	A	---	TGTAACCTGTGTTTCCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGTTTGGAAGACCCATTCTGACTACTAAGGAGAGTCAGCATTCTGACCATTCTGACTGTGCT
WI-22775a	60	A	G	---	TGCTGTTCTTTAGTTCATGACGTTTATCACAATGTGCTACTGTTCCATTGTTTACATC[A/G]TAGTAGGAAAGGGAAAATAAACTCCCTAAGGCAGCAATAATTTCTGTCTTTGAATCCTTCATTCAGGCAAATATTTGTTGAGCACCAAGGGCCAGATGGGAACTGAGGTATGTAGGTGTTGGGAGAAGGAAGGGT
WI-22808	143	C	T	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAGTCCTGAGGGAGCCTAGTCCTCCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGAGGATGAAGA[C/T]AGCAAAACTGATTAAGAGAGTAGGTATAAGAACCAGGGAGAGTGGGGTCCAAATATC
WI-21016	207	G	A	---	TCTCTCGTGTCTTGAGCCCTCATCCCCACCCCTCCAAGCCCTCCAAGTCCAATTCAAGGCCAGACCCTGGCAGCTTTCTGCCCCATCCTCCCCGTCTGCTCCCCATCTCAAGTCCATCGGAGACAGCATGAAAAGGAGGGAGTGGAGCCAGATGGGTGGAGCCAGGTGCGCTGTGGGTCCT[G/A]TTGGGCGTGGTGATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31	C	T	---	TTGAACACCTGACCTGACCTGTGG[C/T]TCTCTGGTCCCCATTTGTCTCCAACGGTGGCACATCTTCATCTTTGTTATATATCTGCGAGAACACTCAGTCTTCTCAGCACGCCGAGAAAAACACACA
WI-21314	122	A	T	---	CCATATCCAGTCTTCTTTGAAGCTTCTATTGACTTTAGGGTTCAGTTATTATATCCTTTATCACTATGACTTTCATTTGATTTTTATTTGTTCTTCCCATTTCTCTGTCAAACTTTTC[A/T]TTTTGTTTATAAACTGTTTTCTAAACTTCACTTAATTCTCTATCTGTATTTNCTTGTAGTTCCCTGAACTTCTTTTAGAGG
WI-21186	95	G	A	---	AGCGGAGCATCAGAATCACCTAGAGGGTTGACTAAAACAGACTTCTGGACCAAACCCCCAGAGCTTCTGATTCAGTAGGCCTGAGGTGGGGCCTTAC[G/A]AATTAGTATTTCGAAGAGCCTTCCTAAGTGTTGCAGATGCTGCTTGTCCCGGGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCCTTTCTTTTAAAGGAGAGACAGGAGAATTCCAGAGAAACTGCTAATTTAAGCATAAATGTATTGAAT
WI-21187a	94	A	G	---	CCACGATAACTATAAAAGCAGAAAAATTAGCTTTGAAAATCAAATAACATATTTAGTAACACACATTCATTTTATAAAACACACATAAAGACACC[A/G]GGNTCCAGTAATGCTCTAGTCCAGGGGTTCTCAAAGTATGGCTTCAGACGATCTGAATCAGAAACTCTGAGCGGTGAGACCAAGCAACCTGTCTACCTACTGATCTACTGAATCAGAAACTCTGATGGGTGAGACCAAGCAACCTGT

ID	Pos	Allele		Sequence
WI-21190	39	T	C	TTTTCCCCACATACCAATGCACCTGTTGTATAAAACTAT[T/C]GTGTGGGTAAGCCCTTCTTTGGAGACCAGTGACATAGACATGATTCCCATTATTATAACAAATAATTATTAATAATCTGTACTATTACTGCTTTAGTTATCTAGTGTTGTTATTGAGAAAGGAGGAGTCAGCATAGTTTATTTTCCATGTAATAAAAGCTTAACACA
WI-19937d	186	G	A	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCAANCTAAACTTGGAAGGAAAGAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCTGTAAAGGTGTTCTATGGCAACAGTGACGATGACATTGGTGTGTTCCTCAGCAAGTC[G/A]TCCAAACCTTCCAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCCTCAGGAAGAA
WI-19937c	185	C	T	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCAANCTAAACTTGGAAGGAAAGAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCTGTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGTC[C/T]GTCCAAACCTTCCAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCCTCAGGAAGAA
WI-21117b	227	C	T	GAAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACTGAAAATCTGTTCAGTTTCACAGGCTCTCTCCAGAAAAATGCATATGTACCAATTGCATGTAGCAATTTCAGAGCCTTCAAATACATTCTGGGGTCCAATCACATACTTCAGGTTCAGAGACTCCCAATATTCCTACAGTTCTGAAGANTAGCAGTCCTCTCATTTCTACAGTCTGTATT[C/T]TTCTACTGAATCTTGGGTGGGAG
WI-21122a	42	C	T	TCACTTTGATCATAATCCCTGTAAAAGCTAAAGTTATTCA[C/T]TTAACAGGAACTCTGTTTTTCCTTATTCAAATGTCACAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGACAACTGGAAATACTAAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCTTTGTAGGTTTCACAGAGAGCCTATTTGTGGGTGCT
WI-21254	53	A	G	CAGTTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGGAACTATTCCCACAGGAG[A/G]CAAGGAGGAAGCTGTTCTCTGG
WI-21054	23	G	T	AAGGAAACTGCATGGGTACAAAT[G/T]TCCAATTCATACTTAACAGGTGGGAAACGGGTCATTCTTGGCCTGCTCCAGAAACAAGGGGCGGAGTCTATGCACTCCTG
WI-21059b	181	T	C	GGGACCAGGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTCCCACTGAGCCTGGCTGAACTACAGCTGCCAGCATTTCCTGGGCTTGCATTTCCTGGGTCTACTTCACTGAAGTCATTTCTATTC[T/C]ATTGTAGCCAGGGCAAAAAATCCTGGGGAAGAAGAGACATACTTCACTGAAGTCATTTCTATTCTCTATTCTATTGTAGCCAGGGCAAAATGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63	C	T	GGGACCAGGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGG[C/T]TTGAACTACAGCTGCCAGCATTTCCTGGGCTTGCACATCTTAATTTCAAGCTGAAAAATCCTGGGGAAGAAGAGACATACTTCACTGAAGTCATTTCTATTCTATTGTAGCCAGGGCAAAATGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

ID					Sequence
WI-20442	37	T	C	---	TCCACGTGTGAAGAAGAAGAAAAAAAANGGGGGGGGGCT[T/C]TAAGGTGGCACAATTTAAGAAAATACCATCCATTTTCTCAGTCTCAATCTGAATCCATACATTAAAACAAAAGTGCAAGTGCAAGTGATGAGACGAACA
WI-21235	43	T	C	---	GTGACAAGAGGTGAAGCAAGGACAAGGGACAGCAGGGCCAGTGTC[T/C]CTCGGGCCGATGTTCCAGGGCAAGCTACGTA
WI-22012a	57	T	C	---	ATCAGAAACTGCAAATCTGCACACATGAAAAGACCTGGGGGAATGCCTACACTCTGGAATT[T/C]CATTACATCAACGTTAAATTTGTCCGACCAGTTCTTCATTGCTGATCACTTTGATAATGACAGATCCAACATGAAAACTTCTGAAGCAAATGAATATTTACCTTGCTTTCATGCAAATTAGGGACCAAACTCAAAGGTTTCATCCATGCTGGGACACCAGACATCTAAGGAAATTGTGACAGGGATCTTCT
WI-21149a	167	G	A	---	AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTGGCAAAGATAGTTGACTAAATACCACTAAATAGTGGCTTTTTTTTTTTTAACAATGACCTTATTTTATCTTTAACTTAACTGAGTCTTATATACAGACCTGCCCAACTGGAAAGCTTTACAC[G/A]TGCTTCAGAATGCGGGCAGTATTGCACAATGGTTTGGGGCAGGTCTGTGTTAAACATGGGATGGAACCCCAGGCTCTACCTG
WI-21376b	188	A	G	---	GGTGTCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAGGAAAAAACACTTTCAATGTGTCTTCCATTTGATGAATTTGTTTTCTCTCTTTATCCCGCAAGTGGAGTTCATGTCCTCGGTGAAACCAGACAGTGTGAATCTGTTCCAGCCCAAATCTGCAGCATTAGGGATGAGTTCTC[A/G]GAAGTGATTCTGAACTGAGCAGCGCACTCATGTCTGTCGGGGAGAAGAGCCT
WI-21382d	125	C	G	---	CCATTGCAGTCCAGAGATGAGAAACTGACCAGAGGCAAATCATGAACAGAAACGGGAGTCAAGAGAAGGGGTTTCTAAGATGGAGAAGTGGGGCGGGTTTGGATCCAGTGGGATNTGGCTTCCC[C/G]AGGTTGCAACCCCAGGAGTCTCTGGAAGCAGCACCAGTCCTGAAGCAGGAGAGCTGCCATCCTCAGTCAGGGTCCGAGTCAGGGTCAGGGAGGAGGAGCTGCTCCATAGTCTCGCAC
WI-21437a	201	G	A	---	TCCCTGAGGTTGGAGTCCTAGCATAGCTCCCCTCCCCTCAAAGAGGGACAAGGGGTCAGGGGCAGAGCAAAAATCCAGTCTGCTTCAACCACGGAGACTGCCTTTGGGATGGAAAGTTTCTGGAGCTCCCTCCATTCTATTCCTGTGGGGCAGGAGAACATGCCAGGCGTCTGCTGGTAAATGCCAGGGGTCACCTTTACCAGGGC[G/A]CAGGCATAGTGGTGGCCCCTGNCTGCCCTGGGGACCCTGGGAACAGT
WI-21202b	156	A	C	---	CAAAATAGAAATTCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCTGTTTTATGAACATGTATTTATAAAAATGGTCACAATATTTTTAAGTTAACTGATTTATTGAGGGAGGAGGAGAGAGTTGACCAAGTTGACCAAGTCTACACATGCATAGACAGTCCTAAAAGCGTATCTCAAACATGA
WI-21202a	61	T	C	---	CAAAATAGAAATTCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATG[T/C]TGATCTGTTTTATGAACATGTATTTATAAAAATTTTTAAGTTAACTGATTTATTGAGGGAGGAGGAGAGAGTTGACCAAAGTCTACACATGCATAGACAGTCCTAAAAGCGTATCTCAAACATGA

				Sequence
WI-21627b	153	A	G	GCATGAAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCATTATGGATATTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATATAAACCATATTTAAAAATGTGTTGAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTTGCTTA
WI-21627a	106	A	G	GCATGAAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTTGCTTA
WI-21399a	75	C	T	GGATTTGAGTCCCAAACTTGATCTCAAATTCACTTCTTGCATGTAAACAAGCTCATTCCCTCTAAAGTT TCAGTTT[C/T]TTCACCCAGTAAGGAAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCTTCTGCATTGTCTTCTGGAGGTTGTGTGTCCCTAGGACTAGGATCTCTCTTGCTTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATACTTGT
WI-20329a	68	G	A	CGATGTCTGCTAAGATAGGAGGTTAATTCTTTACATGGTGAGTGGGTCACAGAGACAAGACATCAAT C[G/A]TCTGTTAGCAGCGGAGAGAGAGCACACTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGCTGGCTTCTTAAAAAAACAGTAAAACCAATCAAAAAGAAAAGATTTAGAGGTTCAGACATT AGGAACAAAATGTGGCCAGAGATACCACAGAGCCCTTGAAGGGAAAGGCCTCACT
WI-21249	155	T	C	TTCTGGCATTCAAATGTACATGTAAAATCCAATTTAACAGATCAAAATTGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAGAAACATTATAAAGGTAATT AAAACTCTAGGTGTATACTTA[T/C]ATGGAACTAGTTTATTTCCNATTAACTACTGTTCATTGCGTA AAGTATGTTGTCCCAATTTCAGCGTGTTTTAAGGAATTATAAAACATTGAGA
WI-21504	147	C	T	TGACACAGCATCAATTTCATGAATACTTTGAAAGGGCCATTAGAAAAAATAAAGAGCCAATTTGGGTC ATTTGAGAAAACATTTTCAGCACAATTTACAGTGGGGCACGGGCCGTTCGGCCTCCAGCTGGGTTTCCC AGATGCAACAAT[C/T]GCGGTTCTCGGCTTCTCCACTGGTGGGGGATCGGGGATCGCGCCCTTCGGAGCTCT CAGGG
WI-21242	115	G	A	CTGCACCAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCCTTCCACCTGGCCATGGTGGTGGTGTT CTCTATGGACCGAGCGAGGCCCTGAAACGGGCGGGGACTGAGGAGGGCAGGGAGGAGAAC[G/A]CACTAGCTTGGGGGGTG GGCCACCAGCTTCAGACCCCTT
WI-21475c	181	A	G	TAGCCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCCAGGCTTCTCCACTTGCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGCGTCTTTGGAGAAGGCA[A/G]AAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTTCCCGTTCTCCACCCTATTCCCTGAAG

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WI-21475b	117	A	T	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGCGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTC[A/T]CTTGCTTACTAAGCA CAGCAGTCGAAGCTTGGGACCTGGCGTCTTTGGAGAAGGCAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTTCCCGTTCTCCACCCTATTCCTCCCTGAAG
WI-20893d	207	A	G	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTGTGCCAGGCTTGCTGCAGGG CTGTCTTCGGCGGTTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCATTTCTTCTCTCTTTTTACAATGCAGT TTC[A/G]ACATAACATTGGTAGAGTAAACACAACAAACCACAAGCCTAAATG
WI-20893c	179	T	C	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTGTGCCAGGCTTGCTGCAGGG CTGTCTTCGGCGGTTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCAT[T/C]TTCTTCTCTCTTTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACACAACAAACCACAAGCCTAAATG
WI-19941c	71	C	G	---	GAGCTCAAGGGAAGAGACCCTTACCCAGATAGGGACTAACTGGAGGGGTGGAAGGAAACAAGGTGAAA GGTAT[C/G]GGTCCTGGTGAGACAAAAGCAGGGGCCTGAGAACACAGAGCAAGGTGGGTTTGGAG GGAGCACAGCAGGGGTGCAGGAAGGGAGAGATGGGGGACCATTTCCTATTCCAGTGCATGTCCCCTTAAAT AAACTGGGTACAGGAGCATTNTGGAAGGAGAAACAAGGAGAAGACAAAGCG
WI-21552b	166	C	A	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTTATGAGTATTTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTTACAAAGAA TCCAAGTATACTCTTGATTATTTAAAAATGTA[C/A]AATTAAATTTATTATTGAATTTAGTTACCCC ATTGTGCTATCAAATATTCAATCTTATTCATTCTTTGTAACTATTTATTTGTA
WI-21552a	66	G	A	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTTATGAGTAAATGCGATCTCCTTCACCTCAAGCATTATCCATAGTAGTGTTACAAAG[G/A]TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTATCCATAGTAGTGTTACAAAG AATCCAAGTATACTCTTGATTATTTAAAAATGTACAATTAAATTTATTATTGAATTTAGTTACCCCA TTGTGCTATCAAATATTCAATCTTATTCATTCTTTGTAACTATTTATTTGTA
WI-21512	54	C	G	---	TCCTCGTACTTCATGCTCCCTCCCCTGCCCCCAGAACCTTACAAAAATATTTCTGT[C/G]TAGAGAGGGA AAGAGCTGGTGGCCTGCCTGCTCTGGAGGCAAGTCCAGGTCCGGGAAAGGCACTCGTGGTCGTGATCTGTC TCAGTGATGGGAGGGGCTGCGTCGTGGGGTCCCCAACGCCTCCTCTTCTTTGGGGG TCCAGTACAGGGGCTCGTGCGGGTACAGCTCCTCTTTGGGGG
WI-21513b	192	G	A	---	CACATAGTTTCTCTACAGAAGAGGATGAACTGAAAACTCCTCTAAGGCAGGACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGAATCTTTAATTTTATATTCTCCTTTATATTCTCCAAAAACATTTTAAGATAAAGAGGCAGTGTAA[G/A]AGTAG CTTAGAGGAAAAATATTCACAGTATACCAAAAACATTTAAGATAAAGAGGCAGTGTAA[G/A]AGTAG TATTCTCTACACCACAGTATACACAGTATACAATGATGCCTTCCTGCGAGGTTTAGGAAC

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WI-21514b	133	C	T	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCCTCTCTAGGACTGTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCGAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTTGTCAAGGGTCATAAGGAACT
WI-21514a	100	A	G	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAAACCCCA[A/G]TCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCGAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTTGTCAAGGGTCATAAGGAACT
WI-22020	27	C	G	ATGAAACATGTTGCAGTGCGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGATCATTCTACCTGTATGAGGGTACTT
WI-19576a	113	A	G	TTCATCGGTTCTTAATACAGTACAATCCTTTGTTGAACAAAAGTCACACTGGCAATGATTATTTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATTC[A/G]TCTAGTTCAGTGATTAGT CACAGAAGAANTTAAACATCTGCCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCACGGGGA G
WI-21695a	141	A	C	ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCACTTGGAAGTGACTACACATGGCAATA AGCAGCCTATCTCTCTTTACCAACCAGAAGTTTCTTGGGGCATGTGATGGTAGGCCAGACCCTTTCCAA GGGAATA[A/C]TACTACCTAAGCCTACACTGTGAGAGTCATGTGGAACAAGGCCACAGGC AGTGGGGAGGAAATGTGATGACTTCACTGTTGTTCAGANTTCTAAGGCCCAGCAT
WI-21574a	235	C	T	AAACCCAGAATTTTAGGTACTTTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG TGTAAATATTTGATCTAGCAGCAACTTCCACTGATCCTGGCAGCTCTGACAGCTCTGAACAGCGC TCATCACCTAAAGTGAGAGGAACTTACTGCTATTCTCATTGTGAATGTCCCTCAGATTCACTAGGGAGGCCATT GGGCAGGCCAGGGAACTTACTGCCTACTTCCT[C/T]GTCGTGTCAGGTGGGA
WI-21644c	151	T	A	TGACTGCCAAGATTTAGGCCCCAACTTAGGAGCCAAGGGTCACCTCTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTCACCATAATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTTAACATGTGTTCTCAGC TTGCCTACTGACCACCTTTCCTTTTCTAAATATGGCAACACACAGCAAGTC
WI-21614b	55	G	A	TGTCTTAACCTCAAAAGTCCAAATAAACATATAGACATTTGANTATAGCTATC[G/A]TTTAACA AACCTCATTATGATCACTGTTGCAATTTCAGTCAGTTCACCTAAAATACGGAACCATGACTATTAATAAACA TTTACTGTGTGGGTTGTTGGGGACTGAACATTAAACCTACGTGTATTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGGTCAATGGTATTTGGGCAGTTGGCGTGTGTGTGGG
WI-21615b	151	C	T	GACCGAGAAAAACTGCAAGGCAGGCAATATGATGTTTGTCGAAGTATCCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACACATATTAAAGATAAGGATGGACT CTTTCACTCGAGTTATATC[C/T]AGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCCC TATTCTATATTGGGCAAAGGGAAAAGGGAAAAGGTAGGATGGGTACTGGTACTGTGTGGAAACGGA

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WI-21981	61	T	A	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAAA[T/A]GTCTCCCTATGGTACTGTGATTTCAATAGGGTGTGGGATAAGTAGTGACAACACATGCATGGGATAGACACTCTGTTCTCTCACAGATCCGTGCTTGGGAATTACAGGAACACATAAAAGGATATAATGGATGGGTTATTACTTTTTACATGTGGACAATCTAGTTGTGAGGCGTTAAGGTTAAATTTGG
WI-21660	120	C	T	TCCCAACTAGCCTCTCCAGTATTTAGATGAGGATAGAACAGATACGGTGTAACACGCCCTCTCCACTGCTTACTGTGTGTACCAAGAAGGCAGAAAGCAGCTCACCCAAGCCTAACCTGGCC[C/T]GTCTTTTCAGGCTTCTCAGGATGCCCAGCACATACTGGGGAACTGGGATGCAGGGAGAGCCAGGGTCTGTCTTCAGGAGGGGTCACAGC
WI-19105c	211	C	T	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGACACTAAGGCACACATGGCCTGGGTGGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTTGTCGTGTAGGTTTCCAGGGCTGGGCACAGAGGGCAGAATNTTGGGGGTCCCAGTGGATCTCCCCACAACTT[C/T]TTCCAGGGGCAGGATTTCCACCCAGGGCCCCAGGGTGCCCG
WI-19105a	33	T	C	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATT[T/C]GTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGGTGGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTTGTCTGTGTAGGTTTCCAGGGCTGGGCACAGAGGGCAGAATNTTCCACCCAGGGCCCCAGGGTGCCCG
WI-21760c	81	C	A	CAAACCTAGTCACTCTACTGATGCAAATGATTGGAGGTGTCTTCCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35	A	G	CAAACCTAGTCACTCTACTGATGCAAATGATTGG[A/G]GGTGTCTTCCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCACCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198	T	C	TCTGCCCATATTGTTCCCAGCACCACTATTACTGTTATTATTCTCTTGAGGAAAACCAGGNATTAAGAAATCTGGTTGAATTTCCATGATGCCTAACCTCTATGGTTAAAAATCCTTTCCTTACCAAAAGGAACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTAC[T/C]AGAGACAAATTCATAGTTCATAATCTTTCAGGGTTGTGCTTTACTTGGGGGGC
WI-20934a	72	T	G	CCAACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCAGAGAA[T/G]TCTAAGACAAATGGTCAAATATTCAAATGGCCTGGCACTAGTGGTAATTCCAGCAGACAAACAGCATGAGAAAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTGCCAATGAGTTACCCAATCAAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAGACCCTNTTCCCCAGGAGA
WI-21561	55	T	G	TTTCCATTTTATTCAGCCGGGCCATCAGAACAATAGCATCTATACCTTCGAAACC[T/G]CCTCTTAACCTCTCCCAGGCAAAGAAGGAAGAAAGTGATCATATTGAATTCCTCAGAATGGTGGGATCTCAAGACTTTTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAAATATAAATGATGATAAATGGTTAGCCTTTCTGGAATAATTTTGTTAATCTGTTTAAAAAGATTTTTGGATGCATTGTCCCCA

ID	Pos	B1	B2		Sequence
WI-21961c	200	T	G	---	AGCTTTGCTTGAAAATTTGGTACTTACTACCTTTGCAATTCTCTTATTATTATTATTACTTTATTT TTCCGTAAGTTATTGGGGTACAGGAGGTATTTGGTTATATAAGTCCATTGTTGTGATT TTGGTGCACCCATTACCCAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTGCCCCT[T/G]C TCCCACTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC
WI-21961b	73	G	A	---	AGCTTTGCTTGAAAATTTGGTACTTACTACCTTTGCAATTCTCTTATTATTATTATTACTTTATTT TTCC[G/A]TAAGTTATTGGGGTACAGGAGGTATTTGGTTATATAAGTCTTTAGTGGCGATTTGTGTG ATTTTGGTGCACCCATTACCCAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTGCCCCTC TCCCACTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC
WI-21956	26	T	G	---	CCCACTTGGGTCTCTTTCAAGTGAAT[T/G]TTCCTTTCGTTCCTGTTCCTAAAGCCTTTAAAATGAACT TCCATTCCTGTTCCTGTGAAACTTGCCTAGTCTGTTTTTCTGCTTCATGCCCCTCAGTGCGAATTCTTTCTT CTGAGGCGGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGGTTGTGGACCTGTAGTCAGGTAACTC CTATCTCTTCCACCGGTAACAGAGGGGTTACATTATGGGGTCCAGGTT
WI-21966	148	G	A	---	CAAACATACATTATGGCTGCCTTTATTTAAGAAATGTTACTGAGAATCTGTACTGTAACAACATAT TTTGTTAGAAGCATGAGTGAGTGTGTGTGTGTGTGTGCGCGCCGGCCATGGCCACTGAGG GGATTGCAATGGG[G/A]AACAGGATAAAAAGGTATAAAAACTTGGTCCGAAATCTTTGCTTATTAAC CTTGGCCCCTGCTCCTCCACAATGTTTCTACACTTAATTCATAGAGAGGTAGA
WI-21930c	146	G	C	---	TATACTGGTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCA CCTGAGTAGTTACATTGTACCCAACTTGTACCCTTTTATCCCTTACCCTTCCACCCTCCACCCCCAT TTTGAGTCT[G/C]CATAGTCCATTATATCACTCTGTATGCCTTTGCATACCCATAGCTTAACTCCC
WI-21139a	165	T	C	---	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCCAGAGCAGAGGGCTTGGTCAAGTCCCTGTTCTGCCA CTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTCTCTGCTCCTTCTCTGTGAAATGGGTACAA TGTGGGTCAGCAGTAAAGGAACTAATACA[T/C]GTACAGCACTTCAGCACAAAGCCTGGGCACACAG
WI-20317b	217	G	T	---	CACTGCATGGAAATACACAGGTAACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGC TGTTGGTTGTCTGTGGTCATTAAAGACAATGTAAGANTCAGGAGTACTTAAGTGCTAGTGGTTACA AATTTTGTTCTTCTTCAGTTTTTCATTAAGTAAATTCTAATAGATGATATACATATTACTGCAGATAAA ACCATCATCAGAAA[G/T]TATTAAAATTAATTGCATATTTGAGGCTACTCT
WI-22082e	179	G	A	---	CAGGACTTGGTTTGCTGTCCCAACTGCACATAAATGTCCCTTTTTGTTGAGTTATTGGTTGTGTGCG TTTTCCTTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCGTCTTGCTTATCCGGATGACGGAGG GTACACGGGGCGTCCGCTCAGTTCCGCCGAAGGACGTATTC[G/A]CTGAACTGGGACGAGTCTACTC CTCCCCCACAGGAGCCCACGATTTCAAATCCTCTTTGCTGCAACCTCT

WI-22082b	67	C T	---	CAGGACTTGGTTTGCTGTCCCAACTGCACATAAAATGTCCCTTTTTGTTTGTTGAGTTATTGGTTGTGTG[C/T]GTTTTCCTTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGACGAGTCTACTCAGGGTACACGGGGCGTCCGCTCAGTTCCCGCCGAAGGACGTATTCGCTGAACTGGGACGAGTCTACTCCTCCCCACAGGAGCCCACGATTTCAAATCCTCTTTGCTGCAAACTCT
WI-20993	139	A G	---	AACACAAACTCCATGCTCTTCAAGATTCCCACACCCAGATACTAAGACATATTAAAATTTACAGCAATTAAAACAGTGTAGTTTGGTACAAGTGAGTATCAATAACACATATGCAATGATACAAATTAGGGGAAAAAACCCTGGGCTTCT[A/G]TAACAAGTGAGTATTAAAGACAGTATTGCAGAATGGCTTCAGGATTAATTTGATTAATTTAGAGAGAGCTATTTCAGGTCTTCCTAGCTCATCCACACATCACC
WI-21723b	125	A G	---	AAGGCGATTTATTAAATTGATTGGACATACTGTAGGTCAAATAATAATATTTCTGAAGATAACAATTATGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCA[A/G]CAACAGCATGATAAAATAATTCAACTATGTAGAAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATCATT
WI-21723a	82	G A	---	AAGGCGATTTATTAAATTGATTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTATGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCAACAACAGCATGATAAAATAATTCAACTATGTAGAAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATCATT
WI-22132	99	T G	---	CAACAGATGCTTGAGCCAAAAAGCAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTCAACCTTTAATCTGACTTGCCTTTACTATCCTT[T/G]CCCCATTTCTTCTCTAATCTCTTTGCCTTACAATATATTACCTTCTCTAGGTATCACCCTCCTATAGGAATGCCTTCAGTTAATGTCCTGCCCCAAACAATACTAACCCATTGAAGGATAACTATGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	A G	---	TGACAGATCACACCACATTTGTTTGTTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAAGATTCTCTTAAAGAACAACATACACACGTGCACACAC[A/G]AGAGGCAAGTACAAAAATGTAACCCCACCAAAGTGCATGTGAATGAAAGTGCAAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTCTCTCTGCTTCAGGAAAATAAACAGAAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C G	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCTGGCTTGGAAATAACTGAAAAGATTCATTTTCTCTTTGTGTACAAAGGATTCAAAATATTTCACATCTTCCTCTGCCAGTTAAACGTGCCGTGGCTC[C/G]CAATACAACCAAAGCCAAAGCGTAACTTGGCTGCTCAGGAAGGCTGGGGAAGTGCCAGATGGTA
WI-21079c	166	G A	---	AATGAAAAATGCCACCCAGGAGGGTTAACAGCTTGCCATGCATGCCGCCAAAATCAAGTTGTTTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAAATTAAAGCTGTGTTGCTCACTTGTTTACATAACTCAGGCCGCACCCTGAAATATCTGCTAGTGGG[G/A]AAATTTACAACCCACTGACCCATCTCAGCTCAAGCCAGATGGACTATCACCTACACATCTGCCAGGTAAGGTAATAGGCATGGGCAAAT

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WI-21079a	50	G	A	AATGAAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGT[G/A]CGCAAAAATCAAGTTGTTTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAAGCTGTGTTGCTCACTTGTTACATAACTCAGGCACCCTGAAATATCTGTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAAAGCCAGATGACTATCACCTCACCTGCCAGGGGTAATAGGCATGGGCAAAT
WI-22129a	45	T	G	TCTGTAGATTTTAGCCATGCCATATATTTAACTTTAAGGAAAAG[T/G]TTATATAACAGTCATTGCTTGGTAGAATCCAGTGTCTCAATAAGTTAGCTCTAACAGTTAAACATTGAAGTCTTATACCTTATATTTAAATGTTTAGCAATCTCTACTACATTTCAAATATAAATAATTGGTTGCAAATTCCAGNAAAGGGCATTAACCAAACATGGGACTGATCCTGGGGGCTTCCACCTTGACTAAGGTTTTA
WI-21941	79	A	G	TGGAGTTAAGTGGGGCTCTGCTATTCCCCCAAGAAGGACTCGGAAGATGTTGATTCCAGGGCAGGAGTGAGGGGCAGGAC[A/G]GGATGAGGCTCTTGTAAAGTCCAACAGACGGCTCACAGATGCTGGGAGGCTGGGGACTGGCCAGGTTGGGGAGCCTCACCCAGAGAGAGCCTCACTGCATTGACCCCACCACCACTCACCCAGCACACAGGCACACGCAGGGGCACACGCAGCACGNTGCACTCACCAGC
WI-18916b	42	C	T	AATGGCATCCCTGTCGATACCAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACTTCTTGGTACCCGGTTAACTGCCAGGNGGGTGACAGTGCCAGGGCTCGCCCCACTACTGCACGACCTCACCAATGCCACCTTCATA
WI-18916a	35	G	C	AATGGCATCCCTGTCGATACCAAACATCTTCAGCA[G/C]CTCAGCGGCTCCCACTTCTTGGTACCCGGTTAACTGCCAGGNGGGTGACAGTGCCAGGGCTCGCCCCACTACTGCACAGCCTCACCAATGCCACCTTCATA
WI-19828c	200	A	G	TTCCCTTCTCCCCAGAAGAGTGGGCAGAAAAGCTTGTTAACCTCCTCTTTACAGATGAAGAGAAAACAAGATCAGAGGTGCTAAGTGCTGTAGCCTAGTCCCAGGNCTTCTGGCCCCAATTCTGGGTTCTCCCCAAGCCCATGCTTCTTCCCACTTCTTCCTGACCCTCACCACCACCACCAGCCCCTGCCCCTGGGCACTTGACCT...[A/G]CTTTTAATTCTGGAAAAGAAACCCAGCTGCACACTGGGCACTTGACCT
WI-21863b	47	C	T	CACAAGAGTCTGTACAACCTTAGGGACGACACCCCTGCCCCTC[C/T]AGCTGCATGCCACCCTCATATCCCACCCCCCATCCCCAGCCTCCTGCCCCGACACCCCCAGCCTCCCGACGCTCCCTGCTCTCGTTGAAGTATTTTCTCCAAGGCAGGAATGAGTGCTTGATCCAACCACAGCATCT
WI-19860	51	C	G	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTATCTCCCATCCCACATAATTCTGTTTGATTTTGCCATTCACCCATAAAATGGTGGGATCTACCTCCCCTCCTTGCAAATTTGAGCTGGNCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19889b	80	C	T	ACCCAGCTCCTCTTCACCCTCTGGCTTTCAGTAGGCTTGGCTAATGGCCANTGAAACTGCAGGGCAAGAGGAGTGAGGGG[C/T]TACAGCATTTATTTCCCTCTTCACTCCCTGTTAGCTTTGGTAGTGGCGTGTATTTCTCTACTGATAGTTCCTTGCCCACAGTCGTAACTATTGC

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WI-19891c	172	C	G	...	TGTTGGTCTGAGAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGCCCCTCCCCCCCG ACTCCTCTGTCTGTGGAAACGTGGCTTTGNCTCCCAGACACGTGTCAGATGCCAGCTCTCCTCAGCGG AGCTCCCGATCCCTCAATTGCCATCGTCTGACTC[C/G]CGTCTTCCCGGGGCGTGGGGGGCTGCTTGT CAGGCAGGCGGGGGCGGGGGAGGAAGGAAGGAGAGATCCAGGGTCTGTCTG
WI-20155a	81	C	T	...	GCACCTGGTAGGGGTGTAGCTTCCATGGTTCTCCAAGCACGGGCTGTACATTACCCTTAGGCTGACCAT TCCCTTGCGCGGGGG[C/T]GCAAAACTGCTTTGAGGAAATNTCCCAGGAGGAATAAACTAGAAGAGCGC ACCTGCTATTTCACCATACTATGGAGAATACAGCTAATGAAGTGGTGGCAGAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAAGTCTCTCTCTCTGTCCAGTCCCAGAGACAGAGACTTCTC
WI-20270b	91	T	G	...	AGCCATACAAGTCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA[T/G]ACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTCCATCTATATAAATACACAGCTGGGGTGGGGAAGGATGCT GGGTGAICTGITGTTCCCCGCAGAGGGCCTGGGAGGCAGGNGGGTGGTGGGAA
WI-20270a	53	G	A	...	AGCCATACAATGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGC[G/A]TCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACCAGGATTTATACACAGCTGGGGTGGGGAAGGATGCT CGATGATACAAAATATAAAGTATATTCCATCTATATAAATACACAGCTGGGGTGGGGAAGGATGCT GGGTGAICTGITGTTCCCCGCAGAGGGCCTGGGAGGCAGGNGGGTGGTGGGAA
WI-20622	130	T	C	...	CCACTTTCAATATTTTACAAAATGCTCACGCAGCAGCAAATATGAAAAGCTTCAACACTTTCCCTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTTCTGTATCTTAAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTCATATACTTTAATGACATCATTGCCAATACATA CATTATTTTCTNTAACTTTATTTTATTTTTACAATAAGCCAACATCGTCATGCAG
WI-20768b	190	C	T	...	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTCAATCCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCCACCACTCTA CAGGAGAGAGGCTATTTCTGGGGCACCCAGAAGNTCAGCACACTACTGCTGGGA[C/T]CAGGGACTC GTAATTCGCCCTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
WI-20768a	71	C	T	...	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGGCTAACAGGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTCAATCCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCCACCACT CTACAGGAGAGAGGCTATTTCTGGGGCACCCAGAAGNTCAGCACACTACTGCTGGGACTC GTAATTCGCCCTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
WI-21909	153	A	T	...	TGTTTGCTTGTGCCAGGTACTCTACTGCTTTACATAAATTATCTCATTCGTGTCACATCTAACGGCAA CTAAGTATACGCTTACATCTGTAGTGGCACCTAAAATAAGGATATTGGTTGGTCATCTTTAAAGAAA TGTCTTAACATACCAAAG[A/T]AGTGGAATCAATCAAATAAAATATTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACTAAATTTATATTCTATGTGTATGGAAAG

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WI-22202	128	A	G	---	TGTTGCTTGGTTGTTGCTTCTGAAACATATTGGAAACACTGTTTTCATAAGCTGTCCTGACAGTGGCACAAATCCATCCATCTCAGGCCTTTAATAAGGTCATTATGAAATCTGAAATTTCT[A/G]TTAATACTCTGGTGCATTCATCTGCAAAAGCAACTGGCACAACCACTCCTTGCCGGTGCAGCTCTCGGAGAACATCTAATATTGAGTGCTAGTTCTGTGTGCGGAACTTCTCCAGCTCAC
WI-22189	70	C	T	---	CCAAGGATGAAATTTCCACATTTATTTNCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCCTATGAA[C/T]GAGGCGGAGGAATGGGCATGGGCGGCTGCCGGTACCAGCCGTTGTGCTTCCAAAGTACACTATGTGTGGTGGGAGACAAAGGGT
WI-22283	109	T	C	---	GGGGAGGCATCATAGAAAAAAACCCTCAGCCACCAGAAGTTAGGACACATTGTGATTCTCAGCCCACTAACGAGCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCCTCTGGTT[T/C]TTCATTTGCAAAATAAAACCCAGACCGGGTCATCTTCAGTTCCCTTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCATGTATGATTTATCAGTCTCCCTGATGCACTCAACTCAACTCAAGTGCAAAG
WI-22290a	136	C	T	---	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGGGTTTTATGGGCCTCTAAGCACCGGCCAGTAGTGGGGAATGCCACATGCAATGGGTGAGTGGGAATCTCGGGGGGGTCAGGGACCTTGCTTTT[C/T]TTCCAATCTCTCCTTCTTAGCCAGGAACTTTGCGAGAGCCCTTTNATTTCTCTCCCTCTATTCCCCTCCTTTCCCCAAATGTCTAAGGTCCAAATTCCCAGACCCCTCCCAG
WI-22292	53	A	G	---	CCAGTGGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATTGCTGAGGTCCCAGTACCAGA[A/G]GTTTGAGTACGGTCGTTTAAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186	C	T	---	ACCTTGCACACCTGCCATCCGGTGCCATCTCCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAGGCTTGTCAACCAAAATGGGCAGCTGGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTTTCACTTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAAGGCAGGATTGTGGT[C/T]CCTTGTGTTTTCTGAACAGGGCCCAGGCAGCCAAGGCATGCCATCCACTGCGAGCACTCAACCCT
WI-22395b	127	A	G	---	GCCCGTTCCAGTATTGATAATAATTGTGTTTAATTTCTATACAGAAATGGTTCTTTCTTGAATATTTGTAGGGATGGGATGAATTGAAAGTGAATTAAAGTCAAGATAAAGGGGCAACTCTTTAAT[A/G]JAAGGAAATGTTACCAAATCCATAGTGAAGAGTAGAAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGGCTCCT
WI-22405	90	A	C	---	TTTATGGCTCCTGAGTGCCTTCACCCAGTACACTTACCTTGTATCTATAAAAGTGTAATTTAGAGTAAATACATTGGCTGTAAAGTCG[A/C]GATCAGGTGCTCTCTCCACCAAAAGCAAAAACAAAACTGCTGAAATTGGCAAGGTTTCTCAGTG
WI-22419b	67	T	C	---	CCCTTCTGGACAGTTGCTTTATGTGTTCAGACAATCAAGGNTCGCCTTCCAGGCACAGCCCAGTGC[T/T/C]CTGGATGGCATCATCAGGCTCCCGCCCCGGCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59	T	C	---	ATTTTCCCTTTCTGTGTTTCGTATTTCCCCTTTTGTCAGTAAATNAGCAATACACTGA[T/C]TGGAAATCTGCATGATTAAATAACAATACATTAACAAGTTCATAAACACACCCCATATCAGAGTAATAAAGCAAGAGGTTGAAAAATATCCCCTAACCGAATGCAAATTAGGTATCCCCTCAAATTGCACATTCTCCTCCTAGTTTT

WI-21763b	154	A	G	---	CATACCCTTTAGGTGCCCACACATTGATCTTAGTTAACAGTCTTGTGTAGTTCCTCTCTTTAGGCTTCAAGA TAATTGTGATTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT GCTCTCCCACAGCTGATT[A/G]CAGACATTGCCTGTGCTTCCTACCCAGCAGCTGTCTAGTGCACTT GA
WI-21763a	135	T	C	---	CATACCCTTTAGGTGCCCACACATTGATCTTAGTTAACAGTCTTGTGTAGTTCCTCTCTTTAGGCTTCAAGA TAATTGTGATTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCAC[T/C]GCTCTCCCACAGCTGATTACAGACATTGCCTGTGCTTCCTACCCAGCAGCTGTCTAGTGCACTT GA
WI-22440	64	A	C	---	CAGTCCATTGAGTCCCAGTCGAGGGTGCATTCTTCCTTTATCTTGCTTAAGCCACTTGGGTA[A/C] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAGAAGTCCCTGGAGGGAGGAGGCTTTCTGG AAAT
WI-22449	74	T	C	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTT[T/C]GAAAAAATACACACAATGGGAACTGACA
WI-21965a	112	A	G	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTGCAGGACCCTGGCTTTCTGCTCCAAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGCC[A/G]CCCCACAGGGTTCTGTT TCCCAAGTCCTGATGGAATTCAGGCAAGACCTTCACACACATTCACCCACTACCTGCTGGAGGAGGGTC ATGAGGCAGCCTGTGGTGCCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115	C	G	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTCCTAGTCAGAAAGTCTCATGGACTTTCCTAAG[C/G]TGTTCTCATGATCAGAC CACCTCCTAAATGTGCTTTACCATTACAGGCTACAGTTGAATCAGGCAGGACGCTGCTGGAG AG
WI-22374a	149	T	C	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAGAATTTCACAACTATTGACTATACAGAG TCTTCAATTCCAAAAAACAGTTAATAGTAACTTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTCAGTAACTAAA[T/C]AGGNTCCTGCATCATTCTCTCACA
WI-22250b	132	C	T	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTGGTTATTATGGGTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATG[C/T] GGANCCAGGAGGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89	G	A	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACT[G/A]TAGTGGGTTATTATGGGGTCTCTGCCTCCTGGTGTTATGC GGANCCAGGAGGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192	G	C	---	GCAGCCATCCTCCTCCAACACCTCCCAGAGCCACCTCGGGGCACCCTCATGCCGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGGCTGGCCCCAGAGGTTCTCGGCGTCTCCAGCAAGTGGA GCCCCAGAGGTTTGCTGGGACTCCAGCCCCAGCCCCAGAACCTG[G/C]AGTGCTTC TTTGACGGCGGCCGCGGCGTCTCCTGCGGGGAGGTGGGGAGGAAGGAGGT

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UTR-04932-2a	149	C	T	---	GCAGCCATCCTCCTCCCACACCTCCCAGGCCACCCTGGGGCCAGAGCACCCTCATGCCAGCAGCAC CTACGTGGCCGCGAGTACGGACCCGCCTGGCCCCAGGTTCTCGGCTTCTCCAGGAGGTCCCAGCCAAGTGGA GCCCAGAGGTTTG[C/T]TGGGACTCCCAGCCAGGGGATGAGCCCCAGAACCTGGAGTGCTTC TTTGACGGGGCGCGGCGTGCTCAGCTGCTCCTGGGAGGTGAGGAAGGAGGT
stFIBBb	412	G	C	---	GTGAGGAAGATGGACCTGGACAGAGCAGTCAGCTCCACACTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGGAGCATGAGCCCTTTCCCACGGCCCTTGCCACTGTCTCCTGGCCCTCTCTGATCATGCCAGG TTTGCACCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGCAGCCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAAACCTTCCATGGTT
stFIBBa	341	T	C	---	GTGAGGAAGATGGACCTGGACAGAGCAGTCAGCTCCACACTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGGAGCATGAGCCCTTTCCCACGGCCCTTGCCACTGTCTCCTGGCCCTCTCTGATCATGCCAGG TTTGCACCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGCAGCCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAAACCTTCCATGGTT
stIGLV2	61	T	C	---	GTCACAAGAGGGCAGCGCTCTCGGGACGTCTCCACCATGGCCTGGGCTCCTCTGCTCCTCAC[T/C]CTC CTCACTCAGGACACAGGTGACGCCCTCACCGGGGCCAGCCACTGACTCACTGGCCATGT TCCTGCTCCTCAGGCTGCAGGAGGGGGTCTTGGGGCTCCTGATCCTTGGTC
stSG10017c	70	T	C	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGCGATCCTCCCACCTCGACCTCCCAGGGTGCTGGGAT TA[T/C]AGGCATGAGCCCCACACCTGGACACAAAATACATTATTATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG10017a	33	G	A	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGC[G/A]ATCCTCCCACCTCGACCTCCCAGGGTGCTGG GATTATAGGCATGAGCCCCACACCTGGACACAAAATACATTATTATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG10023	63	A	T	---	TAATGATAATTAGGGCATTCTTCCCACACGAAGATGACACAATTGACCCAATATCATTGAGGC[A/T] AACAGTTTGGGCTGTTTTCCAGTAGTAGTATGACAGTGA
stSG10096	36	G	C	---	GTGGAGAAAGATCGTCTTTCCTCCCCCATGACC[G/C]GGCTTCCCGCGGGCACCTGTGCGTTTCC ACCCCGAGACGCCCTTTGTAGGGACCCACTGCGCCCACTCCGCTGTGCGCTGGGTTCCGCCTCCTAG GGCTCGAGTGTTTAAG
stSG10118	107	C	A	---	TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCTCCCTGCCTGAGGGCAGTACCCTCCATTGGGC ACAGTCCAGACCAAGTCAAAGATGCCCATTCCTTGCG[C/A]CTCAGCCCTCCAGTTCCTTCATTTCC ACCAGGCCGTGCCCTTGTTGAGTTTTCTCCCCAGTGAG
stSG10120	89	T	C	---	TAGTAGGTAAGAAAAGCAAAGGAGGAATTGCTATGCGGATGACTGTTTACAGTGGTGTCAGACTATGC CGTGTTCACGAACACTTTAATA[T/C]GTT[G/T]GTTGTTAATCTGATTTATCTCGTTCACAAATG
stSG10178	42	C	T	---	TTGAAGCAATATTGTCTAGCACTCTGCTGGACATTAAGTCCG[C/T]GGGAGGAGGAACAGGAA TCGATTCTCTTTGTCTTTAACTGCCCTTAGTTAGGAGATGTTAAAATACTTGGC

Name	Position	Allele 1	Allele 2		Sequence
stSG10193	136	G	A	---	GGAACAATACTACCTAAGGACAAAATACTATTATTAAAAAAAAAGTCTTCTAGTGTATATTGTAACACATTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAACTTTTACTT[G/A]TTGAAAACTGAGAGTTAAGTTGCAAACT
stSG10202c	143	G	T	---	AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGTCTTCCGAGGGAAGCTCAGTCCTGGCTTGCGAGAGTCAGCCTTGGTCACCTCATAACGGGGGCTCCAAGCTCAAGGAAGCAGTCCCACTGCTTCTCGCTGTCA[G/T]CAAGACCACACAAGGCAGATGCCCACTGCCTGTCCTCTTTCCTGTCTTTCT
stSG10209b	75	A	G	---	TCTTTTCTCTTTCACTCTCAGTCACCATGATTCAAATAAACTAATTCTCCTTAAGATCCCACTTATTTA[A/G]CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG10209a	34	C	T	---	TCTTTTCTCTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAATTCTCCTTAAGATCCCACTTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG10218	29	T	C	---	TACTAGACATGCAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTTGTTGACATAATATGCATTGTACCCGGGCATAATAAAGTTAAAAGCCAGTTATTCTGA
stSG10252	108	A	C	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAAAAATGAGAAGAATTCTTTATTTTTGGACCAATTTAGGCACTCAAGAGTTTCTTTCTTTCCCCTTGATCA[A/C]AGTGAAGATGATAGGGAATTCAGAAATTTCTCTTCTTG
EST109150	123	A	C	---	CTGTATTAATTAAGAGAAGGCACTATTAATGAGGGGACGGAAAAATCTACCTGTACACAAAATTCTGTACTTTAACAGCATCTTCAAATAAACCTTAAAGGATAATGGTTTACGATCATTTTAAG[A/C]ATTTTAAGAACTGAGTTATTTGGAC
EST110231	166	T	A	---	TTTTTTGTTAAACCAACCACCCTGAAAGTTTCCACATGTGAAATATAGATACAACAGTGAACAAAATATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAAAACAGCAGGGCAATTAGTCAATTAAAAAAAATAGTACATGTTA[T/A]GTGTAATAAAATTACAAAGGCTTTCCACTCGTGGATTGATTCCTTTTTGGAGGAGGAGTAATCCTGG
EST140968	71	G	C	---	GGGATGTATATTACAGATAACAACAACTCACAAATACCACTCACAAATCTAAGAAAACTAAGGCCATTCTGTGA[G/C]TTATTTTAAAACTTGGTGTTTGCACATAATGATCTTAAAAAAAAAATGAATTACCAAAACCAAGATTCTCTCTAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST221136c	125	C	A	---	TGCAAATTGTGAGAAGGCAGCAGCAGGGGCCAACCCCTGGGACCCTCATCTCTGTCTGTCTAGAATGTGAGGTCGCAGGGATGGCTTAAGTCTTCCTCTGGCAGAGACCCGAGGTGCAGAGAGATGATTCTTCTCAC[C/A]CCCTTCTCTCAGGGTCGTGGAG
EST225557	60	G	A	---	TCAAGCATGTGTAAGGCACTGCCCCGCCCAGACCCTTCTAACTTCTGCACACTGGAAGGT[G/A]AAACCTGGGAGAGAGAAGAGACACTCCCCTCCTAGCTTCGGGCACCCTCCAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

ID	Pos				Sequence
EST22917 6	74	C	T	---	GTAAACCTTGCAAACGCCATGCTGCTAAATGAAGGCCTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAA[C/T]TGACATGGGCGCCAAAAGACTTCCCAGACACAAAGCACGCGAAGGGTAGAGGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65	A	G	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCTCAGGCTGTCTCACTCA[A/ G]TGTGGTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56	A	G	---	GAGGGGGAACTTCAAAGAGGATTCCAACAGTGAAGCAGAATCATGGGGCAAAAGTC[A/G]CTATGG GGCCAGACTGAGGTTGGACCACACAAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
STS-R37410c	201	A	T	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAGAAATCCTCACTTAAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGA ATTTATGGTTTGAATAATACAAAATGTGTATCTCCTGAGACACATTTATAAACATTCTGGTATG T[A/T]TATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R37410b	139	G	T	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAGAAATCCTCACTTAAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGA ATTTTAT[G/T]GTTTGAATAAATACAAAATGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R37410a	48	C	T	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAGAAATCCTCA[C/T]TTAAAAAAAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGA ATTTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R42778	74	C	T	---	TATCGTGGGAAGTTCCAACCTCATACTTATGCTGCTTTCTACTTGCTAATATTGGATGCTTCTTGCCA GGCTC[C/T]TTAAATTGTGCTGTAACCTGGGAAGAAAACCTTCCTACTCTCCACAAACCCTGAA
UTR-04350	125	C	G	---	CAATCTGAAAGAGATGCATAGCGGATTGGTGGCTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGGTTTCCTCCCGGATGGTGAAAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCACGACGACACTGTGAGTGCACTAA
stSG10266	55	T	C	---	GAAATAAAACTAAAACTGCAAAGCAAATCACTGTTAATAAGAATTGTTCTTCTGTT[T/C]GACAGTTG AAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCAATGAGGTCCTCAGAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
stSG10282	70	T	G	---	GTATAATTCAGCATAAGCCAAAGCCTTTTAAAATAACCAATACTATCATTTTATGAAATCTTTACA AGA[T/G]AAGCACAGTAGTACAATATTTAAGCATCTCCAAGTCTCCATTTAAGAGTTGACTATC
stSG10310	128	C	A	---	CACTTTAGATATGAGGAAAATGGTTTAATGGACAACAAAGAGAGTCAGCCACGTTGGAACCAACATAG TTTCATCACCACGTTGAAACCATGTTGTGTATATGCAAATAACAGCAAATAATTTTCACT[C/A]TTG TCAATGCCAATGCATTGAAAGGCCCAGAAATGAGAAAAATGAGAAAAGGATAACAAACTTTGATAAAAAGGTA AGAATTCTGTGTG

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stSG1033 1b	116	T	C	---	TTTAAAGCTACATGTCTCTGAAAGAATGATGCTGCTGATTGAAATAAAGCAACACCTCCA[T/C]GCATTTCCTCTTGG GCTCCAACCTGTCCTGGAGGCCTAGACCTCAAACACCTCCAGCTCTCTGCCCTGCCTTCCACCTGTTCATCTGA CTACTATGTCTTTCCCTGACTTCTGCCTCTCTGGCCTCTCTGCCTGCTTCCACCTGTTCATCTGA CTTAGGACCCTCC
stSG1033 1a	107	A	T	---	TTTAAAGCTACATGTCTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAACCTGTCCTGGAGGCCTAGACCTCAAACACCA[A/T]CACCTCCATGCATTTCCTCTCTTGG CTACTATGTCTTTCCCTGACTTCTGCCTCTCTGGCCTCTCTGCCTGCTTCCACCTGTTCATCTGA CTTAGGACCCTCC
stSG1243 b	225	G	A	---	ATTGGCAAATGGGAAATGACACCAATCATTGATTACAGAAAATGGTTTATAAATCCTCCTCTTG AAATTATGTTCAGGCCCCAGCCACGGTAGCTTATGCCTGCAACTCCAGCACTTCGGGAGGCCAAGGAGGA AGGGATGCCTTGAGCCAGGAGTTGCGACACCAGCCTGGCAACATAGTAAGACCCCATCTCTGTTTT TTTAAAAAAGAAATTCTGTTC[G/A]AAAGTATTTCAGACCAAAGGAGGT
stSG1345 b	60	G	A	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTGAACTAGTTTGCTTCTTAC[G/A]CGCT TCACATTTAGCATGGCCAAAAATTCAGGAGATGCCATGTCCAATGTCCATAAATGGGCAA
stSG1345 a	54	T	G	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTGAACTAGTTTGCT[T/G]CTTACGCGCT TCACATTTAGCATGGCCAAAAATTCAGGAGATGCCATGTCCAATGTCCATAAATGGGCAA
stSG1385 b	117	T	G	---	TTAATGTCATCCAGGAGGGCCAGGGATGGAGGGGGTTGAGGAGGAGGCAGTTATTT TGGGTGGGATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT[T/G]TCAATCATTAAGAA GACAAAGGGTTGTTGAACTTGAACTCGGGGGGGATAGACATGGTATGGCCTCTAAAAAACATGGCC CCAGCAGCTCAGTCCCTTCTCGTCG
stSG139	69	T	C	---	TCGTCTCCTTTCCAGTGCTTCTGCCAGAAGCATCCCAGACTCCACGTGGTCGCTGCTGGTGCTGTACTGTTCTTGTGTCT [T/C]GCTTTGAGCACTGCCCACTCTGGTGCTGCCACTGATTGTGTACTGTTCTTGTGTCCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCTCTCGTCCTCA[T/C]GAGTCTCTCTCCATGTGGCAAACAAGATGGC TGGCTCCTCCACTTGGCTTCTCTGTCCTCAGCTTGGGAAATCAGCAGCAAGAAGAGATGTCTCACTCCCA TACTGTGGTCCCAGGTTCAGTCCTCCTCTCAGCTTGGGAAATCAGCAGCAAGAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTGGGAAG
stSG1427	103	T	C	---	CCCTGGAGTTTCTGAACATAGGAAGGAAGAGAATGCAAGTCATGTTAGGTCC[A/G]CTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAACCCCTTCCTATCCTACC GCA
stSG1471	50	A	G	---	CAAAACCAAAATCCTTCCCACGATATATTACTATTTAGTCTAAG[T/C]TTAATTCAAAGGTTGAGA ATGACGAATTCAAGAATTTCTTCATACATAAATTGCTTCCTTAGTTCTGCAGATGGGTA
stSG1483	44	T	C	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAGTGTGCA [C/G]AATGTGGAGGATGTCTGTTGTTGAGCGTCGTAGTTACTAATGCAGGAAAACCCAATGCAAAGAGGAA
stSG1696	67	C	G	---	AATGCCTGA

ID	Pos				Sequence
stSG1847 b	95	G	A	---	TTGCAGAGACAACAATGGAAGCTTTAAAACCTCTTCAACACAAATGTACCCCTAAAATGAAAGAAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTACTTACATCAGTTGCGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCAATGTGAAAACCAAATTAAAAATAACTTGATCACTGTGCT TCAAACACAACTG
stSG1847 a	49	C	A	---	TTGCAGAGACAACAATGGAAGCTTTAAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTTATAGACATTTGAA ATCATATCTGAATGACTGACTTGTTCCAATGTGAAAACCAAATTAAAAATAACTTGATCACTGTGC TTCAAACACAACTG
stSG1897 a	83	A	G	---	CTTAATGCCCCTTCCTCCTTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACT[A/G]GCCCACCACCTTCCTCCCGGTCTCCCAGATGACT
stSG2022 a	86	T	C	---	TGTCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTATAAAAGTACATTGATCAAGGTACAA TTTTTAACATTAATATACA[T/C]ATTCCATAATCTCATCTATTAACACAGGCCTTTGTTGT TGTTATTTTTTCTCCCTACAATATTCCTGACTCTGTGTAGGGACAGTGGGCCTCAGTTGGGGGGTGAC T
stSG2076 a	104	C	G	---	AAACGTTGTCCCAAAATTGTGTTCAGTTCCACAAGTATAAAATAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTGACATT[C/G]ACATCACAGTGGGGCATTT
stSG2108 c	71	A	G	---	TTGAGCAAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAAATGATTGAGGGGCTCCACAGAGA GAGC[A/G]TAAGGGGAAGACTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGTCTGA
stSG2108 a	49	T	C	---	TTGAGCAAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAAATGATTGAGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGTCTGA
stSG2141 b	173	A	G	---	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGCGATGGTGCAGGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCCTGTTGCTCTG
stSG2141 a	113	C	T	---	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCCTGTTGCTCTG

ID	Pos				Sequence
stSG2148	50	A	G	---	TGGGAAACAACCGGCTATAGTCTGAGTCATATTTTTAGACCGTGATTTC[A/G]AAAGAAAACAATAAATGTGGATTAGAAAGAAACATCCATTACTGTATTTGATACTTGTGATGTTCCAGACGAGCTCATCAC
stSG2175	68	C	T	---	CTCAATGAGGACTCCATCAGCCAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT[C/T]GCCGGCGTGACTCAGCTAATGCTACCGGGGTTGGAGCGCACACCGAGCCCAGCACCTTTCCATACCTGGGCACGAGGGAAGGGAGTGGAAGGACCA
stSG2189	41	C	T	---	CAAGTGGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]TACATTCCCTCCAGTATAATAGGAACTCATCGCTAACTTTGAGCACTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTCCAGCTTTGCGAAC
stSG2200	49	T	C	---	TGTTGATGACCATAGAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/C]TTTATATTTATGTATAATGTCTTACCTGATGATACCCAACATATTACTAGCCTTATAGATGAGGATGGCAGCTTGGCTGGTCAAT
stSG2243	85	G	T	---	CATTTTCTGCCTCCTGCTTCCCAGTACTACCCGTCCAGCAACTGCCTCTCCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCTGATGGTCAGTAGAAAAG[G/T]AGAGCATCTCCTCAAACTCTGTGAGGCTATCAGAAGGGCAG[A/C]CTGTCAGGAACTCTCGCCAAGCACTCTGCCTGTCCTCAGGCAGAATTCTTCCT
stSG2257	65	A	C	---	GTCATCAGCGTAGAGGTCACTGGTATAAACAAACAGTAGCTATATGATATTTACA[A/G]TATGTCCCATTGGGTTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACTGTTTCACAGTTCCTCCAGAGA
stSG2306	67	A	G	---	GAAAACTACCCACCAGCATCATGTTAAAGAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACAAAAAA[T/G]TGCAGTGGAGGGGCTGTGGGAGGGGTGAATG
stSG2334	70	T	G	---	AGAGCAGAATGGTGAATCAACAGACCTCAAATTGTCTTGACTGCGCAGAAGTAACTGCTGTCAC[T/C]GTTCTCAGAGTCACCATTACGGTGACTGTGTCTATTCTGGCTGCTTCCTATTCATCA
stSG2339	63	T	C	---	CAAGACTAAGAAGCCGCACCCGAGTGGTCCCACTCAAAAAAAGAGATTTCTGATTCTACCTCAAAATGCAGAAACCA[C/T]TACAGATTAAAAGAGAAACACACACACTTGAGAAACTCGCCCCTCCTCATCTTCAAAGTGTGGGGTATGCA
stSG2465	76	C	T	---	TTGCAGGCTTGTATTCCACAATAACAAAGTCATGTATAGAGAATGTGAAAGATACTTGAAAACCAAGATATAAAAATATTGAAGTCATTTATGCCTTTTGATGACTGGGTTAAATATGCAAAGCAGCTAAAGGAATAT[T/C]TACACCACCCACCCACCCTTTAACT
stSG2549	140	T	C	---	AATTGCCAAATGGAAAATTCCCAGAGGATTTTTAGACCAACTTTGCCCTGTTGCATTCCCAGTTTGGTCCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/G]GAACAATCCCGGCGCCCAGATTAATTATT
stSG2577b	123	T	G	---	

ID	Pos				Sequence
stSG2577 a	121	C	T	---	AATTGCCAAATGGAAAAATTCCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTCCCAGTTTGGTCCCAATATAGGCCTTCTGCAAGAAGAGAGATCAATGCCGAACCGAACTGTGAAAG[C/T]ATGAACAATCCCGGCCCAGATTAATTATT
stSG2700	58	G	A	---	ATCTCCTGACTGCTTAGTGGGGAAAGGAATCAATTATTTATGAACTGTCCGGCCCC[G/A]AGTCACTCAGCGTTTGCGGGAAAATAAACCACTGGTCCCAGAGCAGAGGCTACTTGAGCGGGACACCA
stSG2724 b	101	T	G	---	AAACAAGCTTTGTCATTTTCCACTACATTTGTTGCTTTATATTAATATTTGCAAATGCTATAATTTAATACTTATATTCCAATTGCTTGCATAATCA[T/G]TTTTTTTAATCCTGGGGTGTTGAAAGAAC
stSG2776 a	65	G	A	---	GTGGCCGATCTTACTTTTCCAGAAAAGGCGGTAAATAAAAACCTGTAGAAAGTCTGAATATGC[G/A]ATTGGCCCTTTGGAGTTAGGCCCAGAACTTCAAACAAGGGACACTGCTGGCCAACCACAAAAATATCCACTAATTCCCGAATATAGTAACCCTGTCTTGTCCGAATG
stSG2791 b	109	G	T	---	AAGGAAAGGTGGAGGGGAAGAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTCTATTATACTTCTGAACGGTAAACTAGCAATTTAATAAATATT[G/T]GGGTCCCACTTAAATCTATTAAAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100	A	G	---	AAGGAAAGGTGGAGGGGAAGAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTCTATTATACTTCTGAACGGTAAACTAGCAATTTA[A/G]TAAATATTGGGGTCCCACTTAAATCTATTAAAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85	C	T	---	CCGCAATTTCAACACACATTCTATGAAAACTAAGGGTGGATCATGTACAACAAAAAACAAGCTCCCTCCCTCCAAAACAAA[C/T]GAACAAAATAAAGAAAATAAAGAAAATGCCCAGGTTTAATTTTTTCC
stSG2850	88	G	A	---	ATGGGTGCATTGTAAAAGGCAAATTAAATACTTTTTCAGGCAGGGCTGGCAAATTTAATGAGCTGATGTGTCCCAAGGGAGACAGGGCCC[G/A]AGGCTCACACATCCCATCAAATACTCCTCCCAT
stSG3031	71	T	C	---	ATACTCACGGGGCTGAAGGCAATGTGAAGGGTCGAAGTCCTGGCCATTTCTGTGGTGTCAGCAAA[T/C]CGCCCTTTATTTAAATGATTCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G	A	---	GTCCCAACTCCTCTCCTCTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG[G/A]AGAAGAAGCATCAAAGGCAAAACTGGCTGAGGC
stSG3092	94	T	G	---	CAGCATCTTCCAGAACATTCCTAGAACTGAACCATTCTTGTCACTATTGAAAAACAAAGCCAAGTTCCAAATCCAAAAATAAATAAAATGAACGTGC[T/G]GATAAACATTCTTCTTATGGTTCCAGCCCTACTTT
stSG3230	95	A	G	---	AAGAAGTACTTTGGTAGCTATTTAAAATAGAGGGGGGTGGGAATGAATGTCGAGATACGAGCACCTGCATCTTTAGTCAATTGTCAGTGGAGTC[A/G]GTGGGGTGCTAAGTGTTCTGAACTGAAGTAG
stSG3245	160	G	C	---	ACATCTCATACCCAGTAAGATGCAAGAAAAGGAAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCCCCAGGTATGTGTAGAGGCCCAGTGGGGTGGCCACTGGTGTTTCTACCACCCCTGGTGTTTCTACCACCCCTGCCATCCAGTCTGGCCCCAGTGACTACCTGGGGAGGTTG[G/C]TTGTACTTGGCTTAAGTACTTCATGTCTTTAT

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stSG3265	42	T	C	---	AGGTGAAATGAGTTACTAAATGTAGCATTATTTATAAGGAAT[T/C]GCATTGTGAATAGTTTCTCAG TTTTCATTATGGAAAGATGATGATTTCAGCCCACATTCAGTGTATGTTTCTAAATAAACACAATCGAC AGGACTGTCTGTTCAGCTGATTTCTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141	C	T	---	ATCTGTCTTGTCAGCTGATTCCTATCCATTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG TGTACTTACTGTGTCATCCTATCCATTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGTGAAGGGAGGAGTCCTCCCAAGTTACCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT GCATGA[C/T]TGTAGATCCCCAAGTCCCTGACACATTTCTTCTAAGAAACT
stSG3269 a	24	A	G	---	TGTACTTACTGTGTCATCCTATCC[A/G]TTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCCTCCCAAGTTACCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCGTGACAGTCCCTGACACATTTCTTCTAAGAAACT
stSG3284	130	C	T	---	TTAACTCAAGAACTTTCAGTTACAGGAAGAGATTTATCTAATATTAAAATGACTAAATTACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAAACTTTGTTAATTGCTGTAATGGGACATTTGTTGTTTTGATCTACCC
stSG3292	99	A	T	---	GTCTCAAGTGAAATCTGTAAATACATTTTAAGTCTGACTTCAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAAATAGCATTTCCTAACTTCAA
stSG3323	26	C	A	---	TAAATGTCATATCTTAGCTCTCACT[C/A]CCAGTGTATCCATTTTCCCAGCCGTAGAGCTTTTCTG TTTCTGTAGATTGCCTGTCCTGGACATTTGATATAAATGGAGTTGCTATCATGTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATTCCATGCGTCAGTGCTTCATTCCTTTTAA
stSG3369	69	C	T	---	GATCCCCAGTAGTATTATTTTCTAAATTGAACTTGTTTGTGGAAATAAAAATCTGAGGACCACTCAGAG GG[C/T]TATAAGGGAACCCTCTTTGTCTTAGTTCATAAGGACTTTCT
stSG3398	125	G	T	---	CAAGACTGTAAGAAACGTAGGCCTTGTGAGAGTGAAGGAAGGATGCTGAAACTTGCCCAGGACTCAGG CTTCAGCTTCACAACTCCCGAGGAAAGGAAATGACATTTCCAAACTGTCACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGAGACAAATAAATAGAGACT
stSG3416 a	43	A	G	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTTGTAGAGACAG
stSG3424	173	T	A	---	GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGTCTTGAACTCCTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTGCTGATATTACAGGTGTGAGCCACTGCCCGCCGACTTTTAAACTGAAT GTTGAAATCATTCTGCTCTTTGCTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCAC TTTCCTTATCTGTAACAAAATGACAAAACAGAACTTTTTCCTTCCTCTC
stSG3436	88	T	A	---	GTTCATGTTAAAGATTAGGAAAGCTGTGAGATGTGATGAGTGTGATGAGGCCTCACAGA ATGAGTGGCAGAGAGGCCCCT[T/A]AGAAATAGCTTACTCTGTTTCCTATC

stSG3463	103	C	T	---	GATACAGAAGATAGTGTGGTATGGATGGATAGTAGTATGAAGGACAAATAATAACAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTCAC[C/T]TGGAACAAACTTGCTTGACTATATTA CTGA
stSG3491 b	71	G	A	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTGCTGGCAAATATTTCTCACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTTGGCACCTGTGGATTTCTATTAAACTCATTTATACTATTTCTGTGATG ACAGAAAATAAGTTAAC
stSG3523	33	C	T	---	TAGCCATCTTACTCTAGTTCTTTTTGGGTTTTA[C/T]GCATATATGTGTGTACAAACACACACACACC CCTAATTCCTCAAATGCTCTTGGCATAAGTTTTATCTCTTACTGGTCTC
stSG3536	213	A	G	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACTACACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCATTCTATTGTTTATATTGTTAAAATGAGCTTG TGCACCATTAG[A/G]TCCTGCTGGGGTGTTCTCAGTCCTTGCCATGAAGTATG
stSG3583	112	G	A	---	GAAAAAGCTTAACATACGATCCATGTGCAAACCCAAAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATCCATGCTGGAAGTGCACCACCACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60	G	C	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAAATCAGGTGTGGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACTCCAGCCTGAGACTGTTTCAAAAA
stSG3589	101	T	C	---	ATATAGTGCTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAAGT GTATATACCACCCTGGCACAAAAAACCCCAATGA[T/C]CCTATTTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590 a	70	A	T	---	GAGAGATGAGCTATTTATTCTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAAA AAA[A/T]TTTCTCTGATGTCTCTGACCCTGTAGGAAACACATTCAGTTCTACACT
stSG3619	78	A	C	---	CAGTGAGACTTCTCATTTATAGCAAATACATTTTGCAGCTAAATTTTCTTGAATTCATATACGCT TCTGTCATTT[A/C]AACAAACTTCCAGAGAAAACTGGGCTCTATATTTAAG
stSG3644	40	T	C	---	ACATATGTAACTGCCATTAGTAGCCATATTTAGGATGAGA[T/C]GATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAAATAATAAGTTATCTGGGGAAACGGCCATTTGTCCAACATTTACTAA GTGCCTACTA
stSG3646 c	70	G	A	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

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stSG3646 b	55	A	G	---	CTCATAATTAGATTGAGAGATTGTGCATTTTGGCAAGAAGAATATATGATGATAACAATA[A/G]TATGTCTTACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATTCTTCTCTTTGTA
stSG3646 a	43	A	T	---	CTCATAATTAGATTGAGAGATTGTGCATTTTGGCAAGAAGAATATATG[A/T]TGATAACAATAATATGTCTTACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATTCTTCTCTTTGTA
stSG3693 b	85	A	C	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCTGGACTCACCTGAAATATCCTACGAGGC[A/C]TGCGCCCTCCGAGACTGACGATTATTAACCACCACACGGAAAAAGG
stSG3693 a	30	C	T	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAACCCTGGACTCACCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAACCACCACACGGAAAAAGG
stSG3698 b	145	G	A	---	TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAATCCCAGGGTTGCTCTCTGACTTCCACCATTCACTGACTTTTATTGCCAGAGGAGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCTTTATTGGGG[G/A]AGAATACCACCACCTTCCCTCACTGCAGA
stSG3698 a	51	C	G	---	TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAATCCCAGGGTTG[C/G]TCTCTGACTTCCACCATTCACTGACTTTTATTGCCAGAGGAGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCTTTATTGGGGAGAATACCACCACCTTCCCTCACTGCAGA
stSG3724	107	C	T	---	ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCCTAGACTTCTGTCTCCCTCACTTCTAAATGAGTGCTCAGTGTCTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAAGTGGCTATGCTGGTGCT
stSG3725	104	G	A	---	GCCAAAACAAAAAGATCTTTGGGAGTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAAATCAAATATATATTATTACCAGCCAACAGCAAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAAATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128	G	A	---	CGGAAGAAAGAAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTTAGAAAGATGATTTTGAGGGCTTCAGTATTTAAAGGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGTCCC[G/A]TTGCTGACTCCATGTTGCAAGAG
stSG3787	49	T	A	---	TTCTGTGCAAAGAATCCACATCATTGTTTGGTAGCAGAGGATCTCTTA[T/A]AAAGTTCCCTAAGACACTGAGGGCATAAAACCAAACAAAATAAAATAAAGGAGTGATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115	G	C	---	GACAAGAGGGAAGAGAGATGCGCCAGAGACCAGGGCTGGGGCGTCCCTGAGTGCCAGGCGCCACCACACGTCTGTGGGTCAAGGCCCCTCCTCGTGGGAGCAGGTCTA[G/C]GCCACGGAGGATGCGAGGGCTGGGAGGGGGACCCCACCCTCGGGGACCCCAAAAGGAGTCCATTTCTGCCCT

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stSG3880 a	36	G	C	---	GACAAGAGGGAAGAGAGATGCGCCAGAGACCAGGGCTG[G/C]GGCAGCTGGGGGTCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTGGGGAGCAGGTCTAGGCAGCAGCAGCAGGGGATGCAG GGCTGGGAGGGGAGCCCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCT
stSG3895	44	A	G	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTT[A/G]TTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTTATCACCATGGTTATCACCATGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902	104	T	C	---	TCTGTTGAGAGACTGGGAGAGAACCAGGTACCAAGCACCAGCACCGACTCGTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCACCTCAACTAAATGTGAACTGCTTTCTTTTC[T/C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGCTCCCTTGCTGGACAAT
stSG3935	50	G	A	---	GGGTGTCTGACGGACAGGCACACCCAGCAGTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCCAGTTCCCACAGCTGAGTACTATGGGGTCACAACCTTCTGGACGT
stSG40	25	A	G	---	GAGGAAGAGGTTGAAGAAGTGCTGA[A/G]AAATATATTTAAGATTTCCTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAAATAAACCCTTGTGATGTATCA CCCAA
stSG4009	32	A	G	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCCTC[A/G]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATTCCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCCACACTGCTTACA
stSG4033	123	T	C	---	AGAAGCCCTTGGGGACAATGGCAGTGCCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAAGAACCTAATGTTTCAAGCATAAAGGTACTT[T/C]TGTGAAC AGGTGGGCAACAC
stSG4038 a	29	G	A	---	GCTGAGAGCAGCAGGTGTACAGCCACGCCTGT[G/A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCCTCAGTCAGGAGGTTCAGGCTCCCGGAGAGCACACTCGAGGGTTCCATCACT
stSG406	53	T	C	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAA[T/C]GGTTTTAGTT TTGCTGAAGACTGCGCCTTATTAATGGACAGCTTTCCTAACAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55	G	T	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG[G/T]ATAAAAAA GTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAAGCCCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27	A	C	---	ATCTGGGCTGAATTAGTCAAGCAGGTC[A/C]GATACTATTGTCTGCTAGATGTATTAGGATAAAAAA GTTTGCTTCTGTGTAATACTTTTAAAGCTTGCTTATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAAGCCCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65	G	A	---	TGCATGTTCCACATCTTTCATAAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G/ A]CTTTTTCCCCTCAGAGCCCTCCAGGACCCACAGTTAAACACGTTCCAGCACCATTAATCCACCGAGCT

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stSG4128	54	A	G	:::	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTCCTTTGTGTACATTTCTT[A/G]TATATTATTTTACTTCTTCTGAAAATGCCACATAATTTGCAATAAATGATTCACTCTCCTTAGCTCCAAAAGCAAGTCCTTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128	G	A	:::	CACGAAACAGATGCAGCCTCACACAGTGCTGTAGGACGAGGCTCACAAACATCCACATGGCACAAGCAGGGCCGGCCACTCCAGGCAAACGAAGCCACCCCCGAACCTTGCAGAGGCCGCACTCCCTC[G/A]GCAGGGGGACCACGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65	G	A	:::	CACGAAACAGATGCAGCCTCACACAGTGCTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G/A]CAGGGGCGGCCACTCCAGGCAAACGAAGCCACCCCGAACCTTGCAGAGGCCCGCACTCCCTCGGCAGGGGGACCACGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31	G	A	:::	CATTACCCAGAACGCCATGGAGGACCAGAGC[G/A]CCACGCGCCGGGGACTCCCGCGATGGCTGGGGGGGCTATGGCCTCTGACAAGAGGATGAGCGGAGGGGCTGCCTCCTCCCCCCAGGGGGCAGAGACGGTGACTGGGGGGACCATGCCGAAGAGAGGATGACCCGGTCATG
stSG4301	81	T	G	:::	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCCACACTTTCCATTTAAGCAAATAAAT[T/G]AGCTTCTGAGTAGTTGTTCCCAGTTCACCCAACATTTG
stSG4331 b	71	T	G	:::	CTCACAAAGGCCAACACAGAGAAAAAGATACAAATACATTCATCCAGCTAATATTTAGTTTTATGACACAGAG[T/G]TTTCAAACAAGTTAAGTGTCACCTGAAGAGCATGTTAAAAGTTTAAGTTTATCACTTGGAGAGCAGATTTCTTGGCCTCGCCCTTGTGATTCTGTTTCTGTTTGAGGGGTGTGC
stSG4340	76	G	A	:::	TTTTGCAACAACATGGATGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACCACATGTTCTC[G/A]TAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109	A	C	:::	TTCCCAACCATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCACAAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGC[A/C]CCTTCACAACTAGAAACGACTCAGCGACTTTTTCTGTGAGCAAATGTCGAGG
stSG4361 a	24	T	C	:::	TTCCCAACCATTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCACAAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACTAGAAACGACTCAGCGACTTTTTCTGTGAGCAAATGTCGAGG
stSG4376	73	A	G	:::	TTTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCTGCAAACTCTGCTTTGCAAAGCCATTCTTCCAAAGCCATTCTTCTTCTCCAGGGGAGAACAG[A/G]GCTGGAACTGCGGGCTCTGCAAACTCCATAGCCAGAGAATGACAACATACGATTTCTT[T/C]TCAGTCTTGTAGT
stSG4381	50	T	C	:::	GAAGGCCACAAACACTCCATAGCCAGAGAATGACAACATACGATTTCTTTCT[T/C]CAGTCTTGTAGTATCCACAGTAGTGATGTCTGTCCATGTGTCCATGTACAAGTGTGTCCATTAAATTCCATGCC
stSG4410	79	A	G	:::	ACCAATGGTTCTGCTATGTGCATCGATATTTTTGCCCGATCTGAAATACTGCAAGGGCTTAACCATTCAAACACCGCG[A/G]TGACAACGAACCCAGTGGACTGTGAAAACTCAGGCTGCAGGAGGGTGGCTTGTCAGCTGGGT

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stSG443	65	C	T	:::	AGCAGATCAGTCAGCCCCACTTGTCTCTCTCTCTCTTTAGGGAGAGAGGCTAGGCAGTGAACACATCA[C/T]GTATGCAATGAGAAAATAACCAACTGGTAGGATGGGGGAGGGGAGGGAGGGGAGGAGGAATAGGCAC AAATGGAATTCTATCCTGGCTGTCCTTCTCAGGTC
stSG4430 a	54	A	G	:::	ATGCACATTAAATGAATGGCCTAACTACTGGGAACTTTAGTAGTTCTATAAGGT[A/G]ATTAACATA GGTAGGATCCAGTTCCTATGACAGGCTTCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTTT
stSG4448	99	G	A	:::	CCTCCCTTCCCTTCCCTTCCCAGTCTTTCCATACTGTTCCCCCTCCCGCCCCCACCCCAGGCTCT CGCCTAGCCCGCCCTCTGGGGTCACTGC[G/A]TGGGTTAGGCCCCCAAAAA
stSG4449	92	T	C	:::	ATTAGCCATTCATCTTGCAACAATTGTCTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT TAACTTTGGACAACTTAAAACTTA[T/C]TAGTGACATTGCTGTCTAATAATCAAATACTTCATCATA GGCTGAACATAATATTAAAAGAGCAAAGTTACCCCTCCC
stSG4467	42	C	A	:::	CAGACAATGAGGGGATGGCCCGTGTCTCTCTGGGACAGAGCCTCA[C/A]AGATGATGTCCATGTTTGTGT GAATGAAACTCAAACACTCTTCAGTTTTAGAGTCATTTTCTGGTATCGAGCGACCACCACCGAGGAG CACACCCTGCTTCCAAGGCGTGCTGCCCTTCTGCACACAGT
stSG4475	21	A	C	:::	ACATGTCATTTCCTGACCAGG[A/C]TATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA TTAAGAGACACAAACTGGACTTTGTTTCTTTACTGTAGCACCCAGGTTTCATG
stSG4477	32	A	G	:::	GTAACATTCTGGGGGTGGGGGTGAGACAAACA[A/G]ATGAACCAATAATTAATTACAATTATACATT TCAAGGAGACTTTAATCTAGGTAATGTGAAACGCAGCCATCAATGGTTTGTCAGGAAAAGGGAGA TGAAGTCTTGCTCTGGGGCAACGTTTGGCCTCATTGCAGTCAGACTTGGC
stSG4531	79	C	T	:::	TGAACTCAGCTGGGTGGGGAGCTGCAGCAGGGGCGCGCCCAGATGAGCCGGCGGGGGA CAGCAGGCGGTGCG[C/T]GCCACGTCCTGGCGTTGGTAGAGAGGACATAGGCTGCGCTTGGACTCGATCT GATTCTCATTGACAGCGGGGAGACGCGTGTTGTCATCAA
stSG4550 b	86	G	A	:::	TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGGCACC[G/A]CAATTGGAGGGGAAGGGGGCAGGGGTTTTAGAGAAC
stSG4550 a	85	C	G	:::	TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGGCAC[C/G]GCAATTGGAGGGGAAGGGGGCAGGGGTTTTAGAGAAC
stSG4590	47	A	G	:::	AATCAGGCACAAGCTCGGGAGAGAAGAGCCAACAAAAGCTCTCTGCAC[A/G]ATGGGAGGGGAGGAGAC CATTGAAAAAGGCATCGTTCCTTCCTCATGCCAAGCGGAGCCCTGGCTCCCCACAGGCATGGTCTCCTTG
stSG4623	22	T	C	:::	AATCTGTATCACCCAGCCTGG[T/C]CAATGTACTAGTAGCTTCCACAGGGATTTTTTATACTATTC CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACTCTTTTCAGCCATTGCAGATTCACATTTATCT TAATATTCCTGTTCAAGATGCTCTGGAG
stSG4843	102	A	C	:::	TAAAAAAAAACACACCCCCCAAAAAAAAACACCCAGAAGTTTTTGAGTTTTATGTTTTCAGATTTAAAG GTATTTCTTTCTTTAGCTTCTTAAATTTTGAGTCAT[A/C]ATCAGAAAGTCTTCCCTACTCCAAGGTGA GAAAGGA

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stSG4850 a	38	C	T	GGAATCTAAACTGGGAATGGCCGAGGAGGAGGGGCTC[C/T]GTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGGTGCCTGTCGGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86	A	G	AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTTTCTGTGAGGTCCTGCTTTTGCAGAATGGCCTG CCCCTGGGACTGGAGCAG[A/G]CTTGGGTGAGCTCTAGGTGGGAGGGTGGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104	G	A	ACTGGACTGGCTCGCTTGCTGAGCGGCGTGAGCGGCCGTGGGCTGCGGCTGACCACCTCGCCTCTTCAG AGACTCGCCCGCGGTGACCACGACTACGCTCTGCC[G/A]GTGGGAAAGCAGAAGCAGGACC
stSG4896	112	C	T	AAACAAATCAAACCCAATCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA GGTTGGGGGCAGCGTGAGGAGTGGTGGGGGCTGGCACCTTTCT[C/T]CAGCCACCAGGCCCCCTGAGG AATTAATTGACTG
stSG4932	22	G	A	ACAGTGCCGATGGTTACACAAT[G/A]TTGTAAATGTATTTAATCCCACTTACGAATGATTAAAATGA TAAATCTTATGTTTATTTCATCACTACCAAAAGGCTGTGGGTGCAGGGGTGCTGGTTTCTGGTCCT
stSG4950	24	A	G	TCATGACTCCCAGGAAAAGGTCCT[A/G]TCTTAGCTTCCTCCTCCTACTTCCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136	G	A	AGATACGGGCAAAACACTGGGATGGCTTCCTGACAACTTAAGAGGTCTCCGAGTTATATTCTGGGTT GGGAAACACTGACCACCCAGCCCTTATTCCTTCAAGGACTCAGTCATTGGCAAGGAGGATTCATGAGCC CC[G/A]GTGACACAGATGGGGGCCCTGCTCTATATTCAAC
stSG4961	91	C	T	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGTAGAAAAGGAAAGTA[C/T]AGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72	A	G	ACTGGTGCCTCTCAGCAGATTCAGGGGTCGTGCAGGGCTGGTTACCACAAACTCAGTAGGAGTGCAA GGGCT[A/G]TACCCCCGGAGCTAGACACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTTGCTGTGC AACCTTG
stSG4997	22	T	C	CAAAGGAGGAGTAGGAGCCCCAA[T/C]TTTTAATGGTTTCCTCTCCCCCTCATGCTATTTGATCCAAAAA CTATATACAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGGGAGGCAAGAA GGGGATAGGGGAGAATGGTGATCCAAAAT
stSG6312	37	C	T	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGGCTCCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107	G	A	GCTCTGGTCAAGCAAATTCTCCAGGACAGAAGCAACAAGGACAGTAAACACACATGTATGACCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC[G/A]ATAGTTCAGGCAATTAAGAATAT GCAAACCCAGAGAATTCTGTGAAAACATTTGCTCTTGGCCTGGTGGTGGACAGAAAGGGGTGGCCAA ATGGGATTGAGTGAGTGATGAGCAGACATG

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stSG6362	88	G	C	TGTGAAATGTACACTCAGGTCTCAACAAATACCTATTATTTCTCTGGTTAAGAAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAGGAAGCAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62	G	T	CACATCTGTGTTTCTGGAGCAAAGGGGAAACCACAGAAGGCCAGGAAGTTTGGGTGTGCACTGG[G/T]T GTCTTTCAACTGGGTGGGAACCAAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAAGAATAGA TGGCTT
stSG8022	53	G	A	AGCTCCTGACTCCCTGTTCAGTGACGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAAAACTGGAAAACTCTACAAATCAATGCGTTATTTCTTATTTCAGAGGCAGGTT TATCAGCACACGCTGTATCTCC
stSG8032	67	G	C	TGATTGTTAGGGATAAGTGGGCATTGTTGTTTACAAATTACTTCCAAAGAATTCAGAAAATTGTGTGTT[G/C]TGGGAGGGCAGGGTAGCAAGATAAAAAGAGGGAGGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46	C	A	AGCTGGCTCTTCCTTCCTGTGTTCGGGGAGGCTTCACGTCCTCG[C/A]CCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGGTGGGAAACAATGCCAGGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8064 a	23	G	C	AGCTGGCTCTTCCTTCCTGTGTGCGT[G/C]TTCGGGGAGGCTTCACGTCCTCGCCCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGGTGGGAAACAATGCCAGGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8072	59	A	G	CACCATCATCACATCGAGTAGGCTGAGGAGCAGGAGGGGTGGGCATGGCCGCAGTTGGCCTG[A/G]TGGC AGAGGCAGAAGGAAGTCCGAGTATTAGTGGCCGCCAGTATTAGTGGCCTGTCGTGTGTTCAAA
stSG8100	40	A	G	ATACACCCACACACCCCACTCAACCTTGTATCAAATTCCA[A/G]AAGTGTAACTAAAGTATAAAGAAT ATCATGACTAGTTAAAAGATAGCAAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138	T	C	AAGGCTCCTTGAAAGCATGTTTATTTGTTTCCATTTAACTTGTTCTCAGCTATACTGAAGTATGATT GACAAATAAAACTTGCATATTTGAGATGTACAGTGTGATGATACATGTATATACAATGTGAAA TGA[T/C]TGTCATAATCATCATAATCAATAATTGGTATATTGGTTAGGAAATGTGATGGT
stSG8105	110	A	G	CAGTGGTTCTCAAACTCCAAACTCCAGCGTACACGAGGATGGTCTTGTGCTTGTGTTAATACACAGATGACTAGGCC CACCTGCGCGGAGTTCCTGTTGGAGTCGTAGGCCTGAGAATATTC[A/G]TTTCTAACAAGTTCCCAGGTGA CCCTGAGGCTCTTGGACTGGGGAACATGCTTTGAG
stSG8130 b	96	T	C	GTGTGTACATCATTGGGAATGGAGGAGGGAAATAAATGACTGGATGGTCGCTGCTGCTGTTCAAATT GACATTCCAGACAAGCGGTGCCTGAGCCT[T/C]GTGCCTGTCTTCACAGCACAGTTCC
stSG8130 a	36	C	G	GTGTGTACATCATTGGGAATGGAGGAGGGAAATAAATGA[C/G]TGGATGGTGCGTGCTTTTAAGTTTCA AATTGACATTCCAGACAAGCGGTGCCTGAGCCTGTGCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124	T	A	TTGTGGACTTCAAATTCTTTCCTTCAGATTTTAAAATGACATTATGCATTATGCATGTACATATTTTAAAATTT AGACACATTTAGAGAACAACAACAATTGTGAACACAAATCTAAGAAATGAATGAGATGT[T/A]CTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTGTCAATCCTCTGTCCTGTGTGTGAAGG

Name	Pos	Allele		Sequence
stSG8145a				TTGTGGACTTCAAATTCTTCCTTCAGATTTAAAATGACATTATGCATGTACATATTTTAAAATTTAGACACATTTTAGAGAGAACACAATTGTGAA[C/T]ACAAATCTAAGAAATGAATGAATGAGATGTTCTGAAATCTGATTCAAACACTTACTTAAACTGACTTCTGTCAATCCTCTGTCCTGTGAAGG
stSG8150	97	C	T	...	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGT[A/G]ATAAAATAATAACGGGAATCCTAGGCATTCGTGTTTTTCTATGTTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAATTGGGAAAT
stSG8340	36	A	G	...	AGAGGATTATGGAGAGAGAGCTGGGCAGGATC[C/T]CAACATTATGACCCTGAACCTCCAGAACTGGATTCACTAGAAGGAGAGAGAGAGAAAAACGCTCATCAAAA
stSG8466	30	C	T	...	TGTGTATTGGGTGACTGTAGCCTAAGGATAAATGAAATAAATGACAGCAATGTTATAAGCAGTGGGAGGAGTGAACTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTATTTGAAAG
stSG8466	111	G	A	...	GATCAAGCAGTGCACACGGGTCACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCCAGTACAAGGATCTGCCGGTCTCCCTGCCGTCGGGGGGCCAACCCCGGCTTCCATGAGGCCATTGGGGACGTGCTGCGGCTCTCGGTCTCCTGAACATCTGCACAAAATCGGGCTGC
ESTD-ACE	--	--		...	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTCCCCAGCTCCACCCAGAGAGCCCCTGGGAATTCCAGGGTCACTGTTCCTTCCTGTCTCCCTGTGGGAATCAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCCTCGGCCACTGAGCTGCAGACCCGCAGACCAACTCCTGAGCTTCTGGGCCTCCTGAGTCTGTCCTC
ESTD-ADA	--	--		...	GGGGAGTGACAGCTAGAGCACCAAGGGGGGCCTCTACAGCTGTGTTCTCATGGAGGCAGCAGGCTTCTGCTCATTCTGG
ESTD-AK-168	--	--		...	AATCCCAGCACTTTAGGGAGGCTGAGGCAGGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGCATGCCTGTAATCCCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCGGAAGGTTGTGTGAGCCGAGATGGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTC
ESTD-ALB	--	--		...	TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCATGGACTGCCCAACTGCGAAACAAGAAGGGCGCAGTGGTGCGAGCAGGAGTATTATGCTACGCGGTTACCTTTTTTTATGGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-ANT1	--	--		...	CCAGGTGTTGTGGCCACGTGCCTGTAATCCCAGCTACTCGGGGAGGACTGAGGCATGAGAATCTTTGAACCGGGGAGGCGGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTCGGCGACACATCGCGGCCACTGCACACCGGACACAGCCTTCGGATGGCTTCGCGACGTGTGGAAAACCATCAGTGAAACTCC
ESTD-APOA2	--	--		...	GGAAGAAAATGGAGCCTGTGGGAAGAGAGCCGTCCGAGGGGGTGGCTTTGTTGGCCAAGCCCCTTGCTGAAGCAGCAAGGGCGTGAAGAACCGGGAGCTCATCCACACTCTCTGACTGCGTGCCAACACTCATGAAGCTGGCCAGGGGACCACCAATGCACAAAGCCTCTGGATGGCTTCGACGTGGGAAAACCATCAGTGAAGGAAGCCCATCCCCCAGAATTGAGCTGCTGCATAATATTGACCCAAAC

Name			Sequence
ESTD-AT3a	··	···	AGACCTCAGTTTCCTCTTCTGTAAAAGGGAAGTTTGTTCTTGGATCTCCATGGGCCCAGCCAGCACTGGTGCCCCTGTGTGAGTCGTGTATCAGGTGAGAGGTGGGACCAGGTGGAGAGGGAATTGAAAGGGCATTGGAATTCAGAGACAAAGAGACAGATATTAAGAGCTGGGGAAATGTGG
ESTD-B3AR	··	···	GGCTGCCAGGGGTTCCGTGGGAGGGCGGCCCCTAGCCGGGGCCCCTGCTGGCCGTGCGGTGTCTGGCCACCGTGGGGAGGCAACCTGCTGGTCATCGTGGCCATCGCCCGGACTCCAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGCCCAGCCGACCTGGTGGGACTCCTGGTGCCGCGGGCGCCCACCTTGGCGC
ESTD-BA511	··	···	GGGCAACATAGTGAAACCCCATCTCTACAAAAATTACAAAAATTAGCCAGGTGTGGTAGCAAGTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAGTGAGCCAAGATGGTGGTGCCACTGCA
ESTD-BCL2	··	···	AGCTGGATTATAACTCCTCTTCTTCTCTCGGGGGCCGTGGGGGTGGGGCGAGCTGGGGCGAGAGGTGCCGTTGGCCCCCGTTGCTTTCTCGGAAGGATGGCGCACGCTGGGAGAACAGGGTACGACAACCGGGAGATAGTGATGAAGTACATCATTATAAGCTGTCGCCAGAGGGGCTACGAGTGGGAGGATGTGGGCGCCGCGCCCCGGGGCCCGCCACCGGGCCATCTTCTCCTCCCA
ESTD-BCR	··	···	CAGTGGCTGAGTGGACGATGGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGAGACCAAAGAGAGGTCAGCTTCGTTCGTCCCGGGAAAGGAGGCAGGTGACAAGCTAACTCTGCTTCAAATCAACCATCCGGTGGACACTGTGTGGCGTGCCATCTGCCTGGCACA
ESTD-BRCA1a	··	···	AAGAGAGAAACTAGAAACACAGTTAAAGTGTCTAATAATGCTGAAAGTGTCTGTAGAGATCTGAAAGATCTCATGTTAAGTGGAGAAAGGGTTTGCAAACTGAAACTGTATTTCACTGGTACGGTACTGATTATGGCACTCAGGAAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAAATAAAT
ESTD-BRCA1b	··	···	ACTAAATGTAAGAAAAAATCTGCTAGAGGAAAACTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTTTTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTTGTTCCAGTTCCAGTTGGGCTCCAGTATTAATGAAA
ESTD-BRCA1c	··	···	ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATAAAGGAAGATACTAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGGCGTCCAGAAAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTTCACCCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAAGATGAAGAGCTTCCC
ESTD-C1R	··	···	ACACAGGTGCTGGCACTCGGGGGCTCGGGGATCCTCCTCCCTAATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C6	··	···	CCCAGTCAGTTTGGGGGACAGCCATGACGCTGAGCCTCTGGGTACTCTTCAACCATGCCATTCCATCTAAGCTCTGCAAAAT

Clone	Sequence
ESTD-C7	ATATCGTGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	GGCAAGTTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGAGAGACATCACCTGAATGTTAG GCAGTGCCTAACTGGGGATGGGATGGCAGCAGACAATGGGCAGTGCCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCCTTTCCCGGCCTTCTCTCTCACACAC
ESTD-CB23	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTTCCCGGCCTTCTCTCTCACACATACACAGAGAGCCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTTCCCACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAA
ESTD-CB24	ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCCGAGGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCGGACCACGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGGTGCACAGACCCGCAGCCCCTCAAGGAG
ESTD-CB25	GTTTTCTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCCTTTTCTCCTATCTTTCGCCGTC TCTGCTCTCGAACCAGGGCATGGAGAATCCACGGGACGCACAGGGGGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACACATGTCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGGTCCTGTGTCGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	TTTTCTGTTCCCTGAAGATTGAGCTCCAACCCCCAAGTACGAAATAGGCTAAACCAATAAAAAAAT TGTGTGTTGGGCCTGGTTGCATTTCAGGAGTTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCAATGCTGCT TTCTCCTGTTCATCCTGATGGAAGTCCTCAAACACCATTCCATACC
ESTD-COL2A1c	AGAATGTATATAGTCCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATAGTTGCTATTTATGCTCTCTTCCTGTCACTTTCAGGGTGTTCAAGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCCTCCGGCTTCCCAGGTAAGTCAAGCATATACAATACTGCCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d	TGAGAGAACACCTAGTCCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACACTGACTTCTTCTACTGCAGCAGCAAGACTTACCC AAGAGAGATTAATGGCAAAGATATACAATACAATTTTATTTGACCAAAACACTATCCATGGAACAGC ATT
ESTD-CPT2	GCCGCAATGCCCGGGGAGTTTCTCCAATGTGTGGAGAAGGCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCCTCCTCATCATGAAAAC TGGGAGGGCGGCCGGGCATAGTGCTCATGCCTGTAATCCCAGCATTTGAGAGGCTGAGGGCGGGGATCAC TTGAGGGTCAGGAGTTTGAGACCAGCCAACCTGGCCAACAT

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ESTD-CTLA-4	ATGGCCTTGCCTTGGATTGCAGCGGCACAAGGCTCAGCTGTGAACCTGGCTACCAGGACCTGGCCCTGCAC TCTCCTGTTTTTTCTTCTCTCATCCGTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCAGCTTGTGTGTGGAGATGCATCTCCAGGCAAAGCCAC
ESTD-CYP2D6	CAGGCCAGCGGTGGTCGAGGTGGTCACCATCCCGGGCAGGAGAACAGGTCAGCCACCACTATGCACAGGT TCTCATCATTGAAGCTGCTCTCAGGGTTCCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD-D11S1873	AAAAAAACATTTTAAACACCTTTCAATCATATACACCATAAATTTCCATTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCATAACTGATTAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCATAT CTGCATGTC
ESTD-D17S33	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCCTCTGACAGATACACTCAGGCGCCGT CATGCTGCACACATCCCAGGGGCGCCCTACCCTTTGTAGTCCTGGAAAGGCTCCTCGGGGCGGGTG GGGTTGTGTGGCTATGTGGCTGTCTTGTGTGAGACGGGGGCTTTGGTTCAGTTGCACTATTGCGTTATT GCAGATTGCTTGTCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD-D18S8	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACACCCTGGCTATCGTAATCCCAGCTACATCGGGAGGCTACATCGGGAGGCAGGAGAATTGCTTGAACCCA GGAGGCAGAGCTTGCGAGTGAGCCAAGATCACCACTGCACTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD-D3S11	AACTGATTAGAAACCTGAAAAATACATATTTTATCTGAAAAAAGTGAGTTATTGGCTCATCACATTGG AATTTTGCATCATCATTAAAAAAATCCAATAAAGTACACTGTAATAAGAATATCCATTGT TTATTCAAACTATTATCACTTATTTATTGGTAAGCCATAAATTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	AGGTTCCACATTATTGCTGATGTTTGCTGAGTGTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACCTTGAGACGTACTTTTCAAAAACTCTCTACAGCGCCGTTGTTGTTATTAATTCAAGGTTGA ACATAAAGTA
ESTD-D3S2	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC TGAGTCTTATTCAAAAACTGACACGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATAATAATCTGTCCTTTATTTGGAAGGATGCCGGTATGT
ESTD-D4S338	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCTATATGGCAGGTATATGAAATGTATTT CTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAATGTATTT TAGCTGTCAGAAAACAAATAACTAATTCTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD-D4S95	CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACTTTCCTTTCTTTTCTTCTTTAGAGTCTACCGG

Name	Sequence
ESTD-D7S399	TGAATCTTAATTGCTATCTCTACAAAATGTATAAAATCCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTTCACAAACATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCCTGGGGACCTCACTGTCCCTGGGGAGAGGAGGGAGGTGGGGAGGGAGGACA GAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGGCCTGTGGGTAGGGCAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGGAGCAGCAGCAGGAGCGAAGAGAACAGAGT
ESTD-DRD1	TCCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCAACCTGAACTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAGAAAACTAAGGTAC
ESTD-DRD2	TCTGCCTTTGGTGCAGGAGGCTGCCCGGGGCAGCCCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCACCCGAGAGGACCCGGTACAGCCCCATCCCACCCGACCCACCCCAGCTGACTCTCCCGGACCCG TCCCACCACGGTCTCCACAGCAACTCCCGACAGCCCCGCCAAACCAGAGAAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCTTTGAGATCCCAATG
ESTD-DRD3	AAGACGATGGCCAGGATGAGCGCGCAGTAGCAGGCATAGTAGTAGGGCATGTGGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACCAGGTGTAGTTCAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCCCAGAGGAGGGTGCGTGATGCCAAGGGGCCTTCCTGTGTGAGGAGA
ESTD-ERBB2	TCTTTCAGGATCCGCATCTGCGCCCTGGTTGGGCATCGCTCCGCTCGGTGTCAGCGGCCTCCACCAGCTGG GGTGAGGGGGTGGTGGGGTCAGTGCCGGGCCGGTGCAGACCCCACGCGGCCTGGGAGGACTTCACCC CGCCCTCACCTCCGTTTCCGTCGCAGCAGTCTCCGCATCGTGTACT
ESTD-ETS2	ACTCACAGTGCTTTAAGTGAAAATGGTCGCTGTTTGGGCTGTTTGGTGCTCTGGAGAAAGAGGCACCAGGAAAGCCGTCCTGGCGCCTGGCA GTCCGTGGGGACGGGGATGGTTCTGGCCTGTTTGCCTTTTGCCTTTGCCTTTTGCAACCAGGAACAGCAAATGCAAAAACTCTTTGAGAGG AGACTATTTTAGATTTTCTTTTGCCTTTTCTTTTGCAACCAGGAACAGCAAATGCAAAAACTCTTTGAGAGG GTAGGAGGGTGGGAAGGAAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCCTCCAAGGCCCGTAGGGGAACTGGGGATCCTAGGGGTGGTGAGCGAATGGCCC AGCCCCAGTCCCCGGCGCCGGTCCCGGTGCCTGGGTCCCAACAGAGGAGGCCGTGGGAGGAGGAGGATGGGGC TGGATGAG
ESTD-F9	AGATCCTGATGATTTTTTCCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAAGTATGATGTTTAAGTCAAACTTCATTTTTTCCATA GGTATGTCCAATTTATCCAGCACAATTTGTTAAAACAAAAAC

ESTD-GCDH	CGCAGACCGGTCAGTGTGGGGTCGGGGAGTGTGGAGGGAAGGAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGGTTCGGCCACCGTCGTTTCTGCTCGCCTGTTCAGCTGCTGTCTGCCCGCAGTCGA GTGTAAGGGACCTCTGGTCGCACCGGTGTGTTCGGTCGTGGCGGTGAAATTCCGAGAGCT CTCTGTCCCGGAAATTCCGAGAGCT
	GTTTTATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGCTCACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAATCCCCCACCACCTGGCTGG AGCAGGAAATGCGAGCGCGCCGCCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG
ESTD-GCK	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCACAGGCATCATTG AAACCAAGTTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-GNAT2	
ESTD-GPPK2L	AGTCTTCATCTGCGGGTGTCCAGGTAGATCCCTTTCACCGCGCCGAGAACTGCTCGATATC
ESTD-HRAS	CTGGGCTCGCCCCGCCGCAGCGTGCTGCCACCTGCGCGGCGGCGGGCAGGCTCACCTCTCTATAGTGGGGGTCG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-HSD3B1	TTGGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGCCCACATTCTGGCCTTG AGGGCCCTGCAGGACCCCCAAGAAGGCCCCAAGCATCCGAGGACAGTTCTACTACTATCTCAGATGACA CGCCTCACCAAAGCTATGATAACCTTAATTACACCCTGAGCAAAGAGTTCGGGCCTCCGGCTTGATTCC AGATGGAGCTTCCTTTATCCCTGATGTATTGGATTGGCTTCCTGCTG
	GGGCTAAAATTTCCGAGCAACTTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGGAGGAAGAGATGTGTTACAGTTTGTCAGAGAGAATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTTCAAAGAAACGGTATACAGGGACAGCA AAGCGCCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT2	ACCAACGAGCGCGCGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGGTGCCTTCTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCCAAGAGTCACTGACAGCTGGCAGGTTCTGCAGCAGGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGGCCGCCGAAGACATGCAGATGTGC
ESTD-HT4	AACACACAAGCCCCAGCGAGGAATTGAACTCGCGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCCTCGTCTGCTGTTTTCTTCCTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAAATTCCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTCGTCTGTAAATCCCTGAAAAGGTTCT
ESTD-HT5	ACCCAGTCGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGGAAGAAGGAAGATGTTC CAGGGCCACACATAGCTTAGTTGGGAGACTC
ESTD-IGFBP1	

ESTD-IGHV4-6	··	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGTCGTGTGAGTGACGGGCAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGAACTGAAAGT ATGTAAATACTTCACAAAATACTAATAAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	··	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATCATTATTATTATTTATTTTTTTG AGATGGAGTCTGGCTCTGTCGTCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGAGTTCACCGT
ESTD-IL1B	··	CCACTTACAGATGGGATAAATGGGTACAATGAAAGGGCCAATAGCCCTCCCTGTCTCTGTATTGAGGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTCAGGGAGCTCTCTGTCAATTGCAGG
ESTD-KRT10	··	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTTGGCAATATT AAAGGAAGAAAAATGCATTTTAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATTACACTGAGATCAACTATGTAGCTGCTTTTTAAATAGTCTC TGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT8	··	ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGGTCAAGGGTCAAGACTAAAGAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCCAGGTTTACCACGTCAACATTGACACA
ESTD-LF79	··	GGGGTGATTTGGAGGCTCAGTTAATATTTCAAAATTGTAACCGTAGCAAAACTGCATTGGTATTTAGA AAAATAAAAAATTTCCAATATGTAGTGCTGTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAGGAGGGCCTTCCCTTACCACCCAGA
ESTD-LMP2	··	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGAGGAATGGAGTTGA CCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	··	TGTCAGGTGTCCCCTAGGGGCACCTCCACCACTCCAGCTCTTCTTCAGCTCTGCGCTCTGCCTGCCTGCTGCA AGGGTTTTGCTTAATTCTCAATTCAATGTCTTCTCATCTTTTAGCAGCTGTGGGGTTTTGTTGTTGTTC TTCTGTTTTTGCTTAGTGATCTGACTACTTTTTTAATTATAAAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATTCAGAAGTTCACAACATTTATTATTATAAAATTTTTCACCTG
ESTD-MCC	··	TTGTCAGGAGTGTGCTGATGCTGCCTCCCCCAGCTCTGTCCCTAGCCGAACTTCAGGACAACGTGCAG
ESTD-METH	··	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAAACAGCATCCCCGAA TCTCAGGAAGTCTCGTGTCTTTCCAAGGGTTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCCTGTGTTTTAGCATGG
ESTD-NF1	··	ATTATCCAGATGAATTTACAAAAACTATACCAGATCCCACAGACTGATATGGCTGGT

ESTD-NFKB1	::	AACATGGACTTGTATATTTGTACAAAAAAAAAGTTTATTTTCTAAAAAAGAAAGAAGAAA AAATTTAAAGGGTGACTTATATCCACACTGCACACTGTGAACTTTTTGTTTGTGAACTTTTTGTTTGTGAACTTTTTGTGGTAGG ATCAGCCCTCATTTGTTGCTTTTGTGAACTTTTTGTAGGGGACGAGAAAGATCATTGAAATTCTGAG AAAACTTCTTTAAACCTCACCTTTGTGGGGTTTTGGAGAAGGTTATCA
ESTD-NPPA	::	TGTCCCTAGGCCCAGCCCTGCTTGTCCTCCCTGGCTGTTATCTTCAGTACTGCAAAGAGAACACAGAC AT
ESTD-NRAMP	::	GGAGGCAGGAGGAGGTGGGGAGGGGGTCTGTCTGCTCCCAGGTCCCACAGACCAGAGAAGCGGCCTCAGTG TATCCCCACCCCAATGTGGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-NRAS	::	GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATATTCTTTCTGCAGGCATATAGAATTTGGT GGGTTTTCTTTTTATGTAGGGTGATATTGGATACTTTTGTTTGTGATTATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGCTTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTGC ATTCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	::	GTGACCTTCTCACTTTAAAAAACTTTACCGGAGAAGAAATTAAATATATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGAGGTATGTAACA
ESTD-PAI1	::	GCCACCACCACCCCACCCCAGCACACCTCCAACCTCAGCCAGCAAGGTTGTTGACACAAAGAGAGCCC TCAGGGGCACAGAGAGTCTGGACAGTGGGGAGTCAGCCGTGTATCATCGGAGGCGGCCGGGCAC ATGGCAGGGGATGAGGGAAAGACCAAGAGAGTCCTCGTTGGGCCCAAGTCCTAGACAGACAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	::	CTCTTCAGGAACCACCAGTCTTCTTACCAAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTCATTAGCTCTGTGAGTGTTTCTTCTGTGTTCTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACTTAGGCTTTCTGTATACCCATGCCC
ESTD-PBDA	::	CCTTCTCATGCCCAGATGGAAATTCCAGTCCCTTCAGGATCGTCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGCTGGGAAGGGCAGGACTAATCCAAATCTCACCCGCAGCTTGCTCGCCATACAGACG GACAGTGTGGTGGGCAACATTGAAAGCCTCGTACC
ESTD-PS-1	::	GGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGGAGACTGGAACACAACCATAGCCTATTCGTAGCCATATTAATTGGTTTGTGCCTTACATT ATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCTCCATCTCCATCTCCATCTTTGGGCTTGTTTT CTACTTTGCCCACAGATTATCTTGTA
ESTD-PXMP1	::	ATGAAACATGGTTCTTTAATTTATGATATGTTTGTTATAGCTATCTTAAAAGGGCTTCTTTTTTA ATGCAGAAAGAGGGGAAAAAAGAGAGCGAGTCGTGGTGGACAAGGTGTGTTTTCTCAAGGCTCATACAGA TTCTGAAAATCATGGTCCCTAGAAACATTTTGTAAAGAGTTAAGTCTTATGAAATTATAATCTT
ESTD-Per/RDS	::	ACCTACAGACGTGCTGGATGTGTGTCCAACCCGAGGAATCTGAGAGCGGAATCGAGAGCGAGAGGCGGCTG CTGGAGAAGAGCGTGCCCGGAGACCTGGAAGGCCT

ESTD-RDS	::	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAGAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCCAAGGGCCAAGGGCCGAGGCGCAGACGCAGG CCAGGCCCCAGAGAGGCGTGGCTGAGGGCCCTGGGGCCCTCCCGAACACTGAGAAATAGTGCACTT CCAAGAAACGTGGATCTCCCCCTCAACTCCGAAAGTCTGAA
ESTD-RYR1	::	CTTCGTGACGGGGAGGTCAGGTCCTCCGCCTCTTCATGGACATATGGATGAGTGTGTGACCATTTCCC CTGCTGACAGTGATGACCAGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGGAGCCACCTGCGGCGGCCAGCCACT CCGAGTCGGCCATGTCACTACGGGCAGTACCCTAGCCGGCTCACCGAGG
ESTD-SPTB	::	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTGTTTCTCCTGGGAGCCTGAGGAGTTTGTGTGTCTGTGTG CAGTCCCCCGGCGCCACCTGCTGGTTGAGCCTGAGCCTGAGCTGGACTACACCTTCACCTCCTTTGGCCCGGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCCCTCTGTGAAGACCCCCAACCCCTGCCTCC CCCACCCCAAGCCAGTTTCCTAGCAAGGGCAGGAC
ESTD-SSA1	::	TTCACTTGTTGGATTGTTTCTTTGCTGTGCGAGCCACCTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCCTGCTCTGTGTGGGATATTGAAAGAGATCTTTGCCAGTCCAATGTCCTAGAGAG TTTTCCCAATGTTTCTTGTTCTTGTAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	::	AAATGGTCAGGACCCTGATCCACACAGAAGTGGTACCATTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAAATGACTTGTGGGACAGGATCA ATTTCCTCTCACCTAGAAACGTTGTTTACAACTTTCTTCCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAATTTAAATAGGACCCCATGAGACACATCA
ESTD-THRB	::	TGCGCGGCCCTTTCCTCCCGGCGAGGGTAGACTTCTTACTTGGCTGTGTTGATTCCAAGAGAGAAAGAGTCCCAAG CACACGAAAAACAGAAGTTGCAGATCCCATGAGGCCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD-TNFA	::	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGGGTCAGCCTCCAGGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGAGACCCCCTCAGAATCGGAGGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCCAACTTTCCCAAATCCCCGCCCCCCGGATGG
ESTD-TYR	::	TAGTGAAGTTTCATCTCCTGTCAGCTTCTTGTTCCCCACCGCAACAAGAAGAGTCTATGC CAAGGCAGAAAAGCTGGTGCTTCATGGCAAAATCAATGTCTCTCCAGATTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTGTTAAACAT GGGTGTTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGATGACA

ESTD-TYRP1	::	AGTAGTGGATGAAGCTAACCAGCCTCCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTTCTTCACTTATTACCTTCTTTCT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACTT
ESTD-VB12	::	TTCCCAAGGCCTCAATACAAGTCTTTTTCTTGGGATTACAACATCAGGGTCTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACAGAGAACACCAGTG ACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	::	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	::	AAGACCTACGTGAATGTTCACATGTGCTTAAAGCCTCCCTTCCTCTCTTACTCTCTGCCTGCTGCAGGATGTG CGACGTGTCGCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCCAGTGAGAAACGCCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD-s14544	::	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST717706		AGCACCACCTCTCAAGCCTCAAGCCTCAGCACCACCAGATGTGTTCTATAAGGATGACGTGCTGTTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAGCTGTTGGTGGAAGG AGTGCCCCAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST524186	::	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCGGCGGGAGTTGGGCGGATACGGGGCTGCAGGCGCATACACTAAAGTGAAAACTGTGAGTGTGG
EST135863	::	CCCACTCTATTTGCCCAGCCCCAGGGACAGAGCTGATCCTTGAACTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCCAGACCCTGCTGCAGACAT AAATAGGCCCTGCAGAGACTGGCTGGCTTAGAGACTGCGAGAAGGAGGTGCGTCCTGCCTGCCCCCG GTCACTC
EST519767	::	AGGCAGAGAAACTGGGCCCCCATGCGGGGGACGTGGAAGGCCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGCAAGACTCTCCCT CCCTGAGCGCTGGAGCAACAGCAGGAACAGCAGGAGCAGCAGGTGCAGATGCTGGCC CCTTTGGAGAGCTGAGCTGCCCCTGGTGC

EST114586	--	---	CCACTTTGGTAGTGCCAGTGTGACTCAGCTCATCCACAATGATTTCTCCAGTGTCGTCCATCGTGCTCATCTTGTTCTCGAGTTTT CTCTGCCAGTGTTGCTATTGCGAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGT CCCATTAAAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST398528	--	---	CGGTCTTCCTTCCAGGTATTGTTGCAGAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAAGGCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST624480	--	---	ACCTGGTGTTGCTGGTGCTGTGGGTGAACCTGGTCCTTGGCATTGCCGGCCCTCCTGGGCGCCCGTGG TCCTCCTGGTGCTGTGGGTAGTCCTGGAGTCAACGGTGCTCCTAGTGAAGCTGGTGCTGATGGCAACC CTGGGAACGATGGTGCTCCCCCAGGTCGCGCGATGGTGCTCAACCCGGTCAACCCGGACACAAGGGAGAGCGCGGGTTACCCTGG CAATAT
EST360272	--	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCAGCATTGCATACACGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCATTCTACAGGGCTCTGCTCTAAAAGACAAATGATTGTTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGTAGATGGCTGCTGCTCTAAAAAGACAAATGAATGGGGAAAGACAA
EST122740	--	---	CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAGAAGTCAAGTGGTTTTACTCCTCATGACCAAATATTCTTCCCTCCTTAGGATGAGGTGAA TAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST768077	--	---	ATGCTAAGGGGGATCGGACATGAAAGGACCCTGTGAGCCGGATTGTCCTATCTCCAGCGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCCAGGTCAGGCCAGCACTGGGCTCCGGAGGACTCACCACTGCGCCCCT GCTGCCATGGTGGCTGGTGCAAGTTGAAGTTGAGGACTTCTTG
EST444387	--	---	GCAGCCAGGAGCCGGCTGCACCATGCCCCGGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGGCGAGCGGAGCCTAAGAGCCGAGGTGGG
EST128393	--	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTACTTATGAATATTATGATACTTAGCTTAG
EST544198	--	---	CTTCTGCCTAATTTGAATGATATGATTATTGTTGCTGTGGGAGACTCGAGCACTTTTATGGCACAAATGATCACTA TTTCTTGACCCCTACTTACAATCCTGGGAGATGTATTTGGGTTTAGCGTGGTGTATGTTGTTCTACTA TAGTCCAAGTGAA

EST103982	--	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGCAACCAGGAGGCTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTCACATTGGGCGTTGACTTTCCAACACGGAGAAG CATTGTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
EST367517	--	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACTCGATACTTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACTTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
		CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCCAAACTTGTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAATAACAAATATTTAACCTTTTGAAAAAATAAATG AAGGAATTTGACCTGCTTCGCTCTGGAAAGAGTATCCGTACCGTCCTGACGTTTTGAAACAATACAGAT GCCTTCCCTTGTGAGCAGTTTTCAGCCTCTCTCACCCTA
EST405562	--	GCTCTCTATACCCGTGTGGTCCTCCCAGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTCATGCAGCGTGTGACAGGATGGAAGACTGGCTGCTCCTGACGGGAGCCAGTGTGG ACAGCACCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST182883	--	TTCCCGCCAGCCGCCCCCCATCCTTGGCACCCTGGTCCCCCTCCAGGGGGCCACCCCCGCGGGGCCACTCACGCTCT CGCTCTCGGTAACATCCGGCGGGGCGGGGCGGGGCCTTCCTGAGCCACACTAGCCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCCTTCCTGTCTGCCCGGCCTTGCCAGGGGCCCTGCAGCGCCCTGCAGAGAGAGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCCACGTG
EST705233	--	CAGTGTATCTGGAAAGCCTACAGGACCACAAAATAAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCCGAGAGACCCAAAATTCCGAGAAGATACACGAGACCGA ATGTATCAAATGACATTCAGCACCATTCAGCAGGAACTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTCTAAGAACCTT
EST587077	--	AGACCATGAAGGAGGTTGAAGGCCTACAAATGGAACAACTGAGCGAACAACTGACCCGGTGGCGGAGG AGACGCGGGCCACGGCTGTCCAAGGAGCTGCAGGAGGTGCGAGGGCCGGCCCCGGCTGGGCGGCGGACATGGGAGGA CGTGCGCGGCGGCGGCCTGGGTGCAGTGCGGCTCCCCACCTGCGCGAGGTGCGCGGCGGCCAGAGCACCGAGGAGC TGCGGGGTGCGGCCTCGCGCCTCCCACCTGCGCGAGGCTGCGGCTAAGCGGCTCCTC
EST741676	--	CGCCTGGTGCAGTACCGGCGGGAGGTGCGAGGTGCAGGCCATGCTGCGGGAGGCACCGAGGACTGCGGGGGTGCG CCTCGCCTCCCACCTGCGCGGCCTGCGGGTAAGCGGCTCCTCCCGCGAGCACCGAGGACTGCGATGACCTGCAGAAGCGCC TGGCAGTGTACCGGCGGCCTGACCAAAAATATACTGGGCGGCCGCCATCCGGGCGGCCGCCACTGTGGGCTG GGGCGCCCTGGTGGAACAGGCGGCGGCGGCGCCCACTGTGGGCTC
EST432118	--	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGGCAGGCTTGGCCAGGTTTGGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTGGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCGATAGGGCTGGCCTGACCAAAAATATACTGGGTTTCCTGTTTTCTGATCAT TCTTACAAGTTATACTCTTATTTGGAAGGCCCTAAAGAAGAGGCTTATG
EST367704	--	

EST26021 1	...	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATTTTGTGAAAGAAGAGGAGCAAGAGAACATTCCTCGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAAACAAAGCTTTTCTTTTCCTTTGCAACAAGACAAAGCAAAGCC
EST51212 0	...	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTCTCTTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCGCCTTGAGGAGCCCTGGAGCCCTTGTGTCTCCCCACTCAATACAAAAAGGCCCCTCTCT ACATCT
EST20118 2	...	GTTCCGAATCCTCCTCTGAAAGTGGCCGGGGTTTAATCTGCTCATGACGCTGCGGGCTGTGGTCCAGCT GAGGTGAGGGGGCCTTGAAGCTGGGAGTGGGGGTTTAGGGACGCGGGGTCTCTGCGTGCATCCTAAGCTCT GAGAGCAAAACCTCCCTTGAAGCTGGGAGTGGGGTTTAGGGAGCTGGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	...	ACAATCCAGGTCACACATTCCAGAAGAGGAGGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	...	CTTCCTATGGGATTTGACTTTATTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTGAAGCTGACAATTACACAAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTCGAAACATTGAAAGTTGTTTTGGTGTCACCTTTAATTACACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
EST34088 2	...	GTGGGGGCCAACAGTGGGGAGAAGGGGCCAGGGTATAAAAGGGGCCCACAAGAGACACGGCTCAAGG ATCCCAAGGCCCCAACTCCCCGAACCACTCCAGGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	...	CTGAGAAACAATTGGCAAAATAAAGGAATTGGCCACTCCCCACCCCCTCTTTCTCTTCTCCCTTGGA CTTTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAAGAGAAGAGACCCCAGAAAT CACAGGTGGGCACGTGCGTCTCACGCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082	...	TCCAGGGGTGGCTGGACCCCAGCTCTCGCAGCAGGAGGACGTGGCTGGGCTCGTGAAGCATG TGGGGGTGAGCCCAGGGCCCCAAGGCCACCTGGCCTCAGCCTCAGCCCTGCCCTGTCAC CCAGATCACTGTCCTTCTCTGCTCTCTGTGATGCGCCCTGCCCCTGCTGGCGGCTGCTGGCCCCTC TGGGGACCTGACCCAGCGCGCAGCCCTTTGTGAACCAACACCTGTGCG
EST45311 0	...	GCCCTCCTCTCTCTTCCAATTCTGTCCCTATAGTTTCCTCTATTAAGTGAACTACACATGCATTCTTTAGT GGATAGATGCACACAAACACACAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCCATATTGTAACA CATTTTCTGCAAATCACCTCTTTCATTTAACAGCCCTTATTCAATGGCCTTTTTCTTTTCAGTAGTA CATACACATCTGTGTCATTTGTTGAAT

EST652588

TGCCCATCACGCGGCCGGAGACATGGCTTGCCACAGCTTCTTGAGGATGTCACCAATTAACCAGAAAT
CCAGTTATTTCCACCCTGACTGGCGGCCGGCCGGTGCTTCTCGTCGCGGGGG
ACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG
GTTAGGTGCGGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA

EST382163

ATGCAGGATGAAGGTGGACAGGGAGGAGGGGCCAACCTGTCATCCCAGGCCTGCAGATGTCGCTG
GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG

EST627829

ATACTAGTACAAGTGGTAATTTGTACATTACACTAAATTATTAGCATTGTTTTAGCATTACCTAA
TTTTTCCTGCTCCAGACTGTTAGCTTTTACCTTAAATGCTTATTTAAAATGACAGTGGAAG
TTTTTTTTTTCCTCGAAGTGCCAGTATTCCCAGAGTTTTGGTTTTTGAACTAGCAATGCCTGTGAAAAA
GAAACTGAATACCTAAGATTTCTGTCTGGGGGTTTTTGGTGCATGCA

EST358799

GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGAATTCTCCCAATCTTGTGCGTTCCACCGATG
GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG
AGAGTTGAACAGATTCCTGGAAGACAGCAGCGGGGCAGGAGAAGAGCTGCCTGGATGAA

EST683085

GGAAAGAGAGATTTAAGAAGCTTGATTTGGACAATTCTCGGTTCTTTGAGTGTGGAAGAGTTCATGTCTCT
GCCTGAGTTACAACAGAATCCTTAGTCACGCGAGTAATAGATATATTCGACACAGATGGGAATGGA
GAAGTAGAACTTTAAAGGTAAGAAAGTAGTATTTTA

EST540456

GGAATATTAAAAATATTTAAAATACCTCCATTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA
AAGACATGGCTAAAGTTATGATGTGTTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAATCT
GTTAAGTAAGTACTGTTTTGCCTTGGAATTGGATTTTTAATGTTGACTTTATCAT

EST529080

ATCACAGGTCTCTCTGGTCTCTGGCCATCATTCCTGGGAGAGATGGATGTGGTCTCGCAAGCCCTTTGG
CAATGTGAGATTTGATG

EST195900

AGGAGAAGCTGAGGAGGGGAAGAGAGAGACAAGAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT
GCCGGAAAATGAC

EST761361

TGAAGCTTCTGCCCAGCTTGCATTGTTCTAGGAGAACCCGGCTCATACCTTTATCTATAGCCTTCCCC
TAGGTCTT

EST586070

CTCTGGATGGGTTCACAGGTGGCAGGCACAGCCAGTCCATCATCCTGTAGTCATCATAGTTGTTGGCTCC
CAAGTTGCTGCTCCTCCACTGGAGACAAGGACAGCCACATGGCGCGGGATGGCCGCGGGGAGTTCTGGT
TGCGGGCCACGGCTGTGGCCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGGATGCCTAAACCTTTGTTTCT
TGGCCAAGGAGGGGCGGGGGGTGCCATGCCTGAGATGTGAGATGCGGCC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table, or a portion thereof which includes a polymorphic site, or the complement of the segment or portion thereof.

2. The nucleic acid segment of claim 1 that is DNA.

3. The nucleic acid segment of claim 1 that is RNA.

4. The segment of claim 1 that is less than 100 bases.

5. The segment of claim 1 that is less than 50 bases.

6. The segment of claim 1 that is less than 20 bases.

7. The segment of claim 1, wherein the polymorphic site is biallelic.

8. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is the reference base for the fragment listed in the Table, column 3.

9. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is an alternative form for the fragment listed in the Table, column 4.

10. An allele-specific oligonucleotide that hybridizes to a segment of a fragment shown in the Table, column 7 or its complement.

11. The allele-specific oligonucleotide of claim 10 that is a probe.

12. The allele-specific oligonucleotide of claim 10, wherein a central position of the probe aligns with the polymorphic site of the fragment.

13. The allele-specific oligonucleotide of claim 10 that is a primer.

14. The allele-specific oligonucleotide of claim 13, wherein the 3' end of the primer aligns with the polymorphic site of the fragment.

15. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 5.

16. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 6.

17. An isolated nucleic acid comprising a sequence of the Table, column 7 or the complement thereof, wherein the polymorphic site within the sequence or complement is occupied by a base other than the reference base shown in the Table, column 3.

18. A method of analyzing a nucleic acid, comprising obtaining the nucleic acid from an individual; and determining a base occupying any one of the polymorphic sites shown in the Table.

19. The method of claim 18, wherein the determining comprises determining a set of bases occupying a set of the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is
    obtained from a plurality of individuals, and a base
    occupying one of the polymorphic positions is
    determined in each of the individuals, and the method
5   further comprising testing each individual for the
    presence of a disease phenotype, and correlating the
    presence of the disease phenotype with the base.